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152102

From: Slobodyansky, Elizabeth
Sent: Friday, April 29, 2005 2:53 PM
To: STIC-Biotech/ChemLib
Subject: 08/952,741 SEQ

CRFE

Please search for case 08/952,741:

es

SEQ ID NOs: 1 and 2 against commercial ~~and interference~~ databases.

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Elizabeth Slobodyansky, PhD

Primary Examiner
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Searcher: _____
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Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 2, 2005, 17:25:37 ; Search time 5173 Seconds
(without alignments)
16635.698 Million cell updates/sec

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Sequence: 1 atataatctgaatgcagaca.....ccaataataatgcgaagctt 1776

Scoring table:
IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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1: gb_da:*
2: gb_hlg:*
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11: gb_str:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1776	100.0	1776	6	AR411953
3	1776	100.0	1776	6	AX453590
4	1776	100.0	1786	1	AB008763 Bacillus
5	1776	100.0	1786	6	BD144003 Alpha-amy
6	1776	100.0	1786	6	ES1838 Variant alp
7	1776	100.0	1786	6	AR541695 Sequence
8	1776	100.0	1786	6	AX428291 Sequence
9	1187.2	66.8	6661	6	AX601433
10	1170	65.9	1458	6	AR087556 Sequence
11	1170	65.9	1458	6	AR224266 Sequence
12	1167	65.7	1455	6	AR027254 Sequence
13	1167	65.7	1455	6	AR049517 Sequence
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ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
E12445	E12445	DNA encoding liquefaction type alkaline alpha amylase from Bacillus sp.	E12445	E12445.1	GI:3251278	JP 1996336392-A/1.	Bacillus sp.	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.	Hatada, Y., Ozaki, K., Ara, K., Kawai, S. and Ito, S.	LIQUERIED-TYPE ALKALI ALPHA-AMYLASE GENE	Patent: JP 1996336392-A 1 24-DEC-1996;	OS Bacillus sp. PN JP 1996336392-A/1 PD 14-DEC-1996 PP 14-JUN-1995 JP 1995147257 PI HATADA YUJUI, OZAKI KATSUYA, ARA KATSUTOSHI, KAWAI SHUJI, ITO SUSUMU PC C12N15/09, C12N9/28; CC strandness: Double; CC topology: linear; CC hypothetical: No; CC anti-sense: No; FH Key FT source FT 1..1776 FT /organism='Bacillus sp.' FT /strain='KSM-AP1378' FT /clone='PAM100' FT 1..144 FT 145..1695 FT /product='liquefaction type alkaline alpha amylase from FT Bacillus sp.' FT 1696..1776 FT 1..31 FT /note='Signal sequences' FT 127..132

FT /note='SD sequences'
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FT -10_signal 31..36
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location/Qualifiers
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1776; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS AR411953
DEFINITION Sequence 1 from patent US 6638748.
ACCESSION AR411953
VERSION AR411953.1 GI:40164465
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.

1 (bases 1 to 1776)

AUTHORS Hatada, Y., Ozaki, K., Ara, K., Kawai, S. and Ito, S.

TITLE Gene encoding alkaline lipolytic alpha-amylase

JOURNAL Patent: US 6638748-A 1 28-Oct-2003;

FEATURES Location/Qualifiers

source 1..1776

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ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1776; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATATTAATTTGAATGAACACTTATGAAAATATGATGCGGAGAGAAAAC 60
 DB 1 ATATTAATTTGAATGAACACTTATGAAAATATGATGCGGAGAGAAAAC 60
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 SOURCE
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 Bacillus sp.
 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

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REFERENCE      1
AUTHORS        Andersen, C.
TITLE          Alpha-amylase variant with altered properties
JOURNAL        Patent: WO 0231124-A 7 18-APR-2002;
                Novozymes A/S (DK)
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Matches 1776; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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  QY      1201 CCTATACATGACATGACATTTGTGTAACATGACCTTCAGCCAGAGAGACATTTGAA
  DB      1201 CCTATACATGACATGACATTTGTGTAACATGACCTTCAGCCAGAGAGACATTTGAA
  QY      1261 TCCTTTGTTCATTCGTGCTTCAACCACTGCAATATGATTTGATTCGACAGAGGACAA
  DB      1261 TCCTTTGTTCATTCGTGCTTCAACCACTGCAATATGATTTGATTCGACAGAGGACAA
  QY      1321 GGTACCTTCGATATTTTACAGGTGATTAACAGGTAACCAACTCAATGATGCTCTTG
  DB      1321 GGTACCTTCGATATTTTACAGGTGATTAACAGGTAACCAACTCAATGATGCTCTTG
  QY      1381 ATGAATCTTAAATATGATCACTTCTGAGGACGTCAGAAAGTATGCTTACGAAACCAA
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  QY      1441 CATGATATTTTGTATCATATGATATTAATGCTGTCAGAGAGAGAGGACAGCTCCAC
  DB      1441 CATGATATTTTGTATCATATGATATTAATGCTGTCAGAGAGAGAGGACAGCTCCAC
  QY      1501 CCAAAATTCAGAGCTTGCACTTATATGTCGATGGGCCAGGGGGTATTAATGATGAT
  DB      1501 CCAAAATTCAGAGCTTGCACTTATATGTCGATGGGCCAGGGGGTATTAATGATGAT
  QY      1561 GTGCGGAAAACATTAAGCTGCGCAAGTATGAGAGATATCACCGAAATAGTCTGTAAC
  DB      1561 GTGCGGAAAACATTAAGCTGCGCAAGTATGAGAGATATCACCGAAATAGTCTGTAAC
  QY      1621 GTGCGGAAAACATTAAGCTGCGCAAGTATGAGAGATATCACCGAAATAGTCTGTAAC
  DB      1621 GTGCGGAAAACATTAAGCTGCGCAAGTATGAGAGATATCACCGAAATAGTCTGTAAC
  QY      1680 GTGCGGAAAACATTAAGCTGCGCAAGTATGAGAGATATCACCGAAATAGTCTGTAAC
  DB      1680 GTGCGGAAAACATTAAGCTGCGCAAGTATGAGAGATATCACCGAAATAGTCTGTAAC

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Qy 1681 TGGGTGAAGCAATTAATGAAGGCAAGGCAAAATTAATTCTTCTCATGACGAGCTTT 1740
Db 1681 TGGGTGAAGCAATTAATGAAGGCAAGGCAAAATTAATTCTTCTCATGACGAGCTTT 1740

Qy 1741 CCGATCACTCATACCCCAATTAATTTGGAAGCTT 1776
Db 1741 CCGATCACTCATACCCCAATTAATTTGGAAGCTT 1776

RESULT 4
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LOCUS
DEFINITION Bacillus sp. gene for amylase, complete cds.
ACCESSION AB008763
VERSION AB008763.1 GI:3445479
KEYWORDS amylase.
SOURCE Bacillus sp.
ORGANISM Bacillus sp.
REFERENCE 1 (bases 1 to 1786)
AUTHORS Igarashi, K., Hatada, Y., Ikawa, K., Araki, H., Ozawa, T., Kobayashi, T., Ozaki, K. and Ito, S.
TITLE Improved thermostability of a Bacillus alpha-amylase by deletion of an arginine-glycine residue is caused by enhanced calcium binding
JOURNAL Biochem. Biophys. Res. Commun. 248 (2), 372-377 (1998)
MEDLINE 98342096
PUBMED 9675143

REFERENCE
AUTHORS Hatada, Y.
TITLE Direct Submission
JOURNAL Submitted (10-NOV-1997) Yuji Hatada, Kao Corporation, Tochigi Research Laboratories; 2606 Akabane, Ichikai, Haga-gun, Tochigi 321-3497, Japan (Tel:0285-68-7400, Fax:0285-68-7403)
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ORIGIN
Query Match 100.0%; Score 1776; DB 1; Length 1786;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1776; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATATTAATTTGAATGAACACCTATGAATAATGTGCGATTGCGGACGAGAAAAAC 60
Db 11 ATATTAATTTGAATGAACACCTATGAATAATGTGCGATTGCGGACGAGAAAAAC 70

Qy 61 TTGGAGTTGAGGAGTGATATTAAGATTTTGTGACTGTGTGAAAAAGCTTGAT 120
Db 71 TTGGAGTTGAGGAGTGATATTAAGATTTTGTGACTGTGTGAAAAAGCTTGAT 130

Qy 121 AAATTGAAGAGAGAGGCTTTTATGAACTTCATACCGTATTAATGAGCTATTA 180
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Qy 181 ACACTATTGTAGCTGAGCTGTTTGTTCATATATGACGGAACGACAGCCAT 240
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Qy 241 CATATATGAGAGAGATGAGACCATGATGATTTGATGCAATTTGCCAATGACGG 300
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Db 311 AACCACTGGAACAGTTACAGATGACGAGCTTAACCTTAAGATTAAGGATTAACGG 370

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Db 371 GTTTGATTCCTCTCGATGAGAGGAGCTTCGCCAATATGATGTGGATGCTTAT 430

Qy 421 GATTTGATGATCTTGTGATGTTTAAACCAAGGGAACGTCCTGTAACAAATATGAC 480
Db 431 GATTTGATGATCTTGTGATGTTTAAACCAAGGGAACGTCCTGTAACAAATATGAC 490

Qy 481 AGGAGTATGTTGCAAGTGCCTGATCATCTTTGAAAAATTAACGGATTTCAAGTT 540
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Qy 541 GATGTGATGATGATCATTAAGGTGAGACGAGGACAGAGATGTTAATGCGTGGAA 600
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Qy 601 GTGAACCGAAGCAACCGAAACCAAGAAATATCAGTGAATATCACTTAAGACATG 660
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Qy 661 AAATTGATTTCCCTGGAAGAGAAATATCCATTTCCATTTAAATGCGCTGATCAT 720
Db 671 AAATTGATTTCCCTGGAAGAGAAATATCCATTTCCATTTAAATGCGCTGATCAT 730

Qy 721 TTTGATGGGACAGATTTGGGATCATGTCAGCTCAGCTTACAGAACAAATATTAAT 780
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Qy 781 GGTAACCGAAGGACATGGGACCTGGGAATGATATGAGAACGCACTATGATTA 840
Db 791 GGTAACCGAAGGACATGGGACCTGGGAATGATATGAGAACGCACTATGATTA 850

Qy 841 ATGATGACAGACATTTGATATGATCATCCAGAAATATCAATGAATTAATTTGG 900
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Qy 901 GTTTGATATCAAAATCACTTATCTAGATGATTAAGATTCGATGCTGGAACATATT 960
Db 911 GTTTGATATCAAAATCACTTATCTAGATGATTAAGATTCGATGCTGGAACATATT 970

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Qy 1021 TTTCAGTTGCAAAATTTGAAAAATGACCTTGCTGCAATGCAATCTATTTAAT 1080
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Qy 1141 AATAGTGTGGCTATTTTGTATGAGAAATATTTAATGTTCTGTGTAACAAACAC 1200
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Qy 1201 CTTATACATGACAGTCACTTTGTTATTAACCATGACTCTGACGACAGAGAACTT 1260
Db 1211 CTTATACATGACAGTCACTTTGTTATTAACCATGACTCTGACGACAGAGAACTT 1270

Qy	1261	TCCTTTGTCGATCGTGGTTCAAAACCCATGGCATATAGCATGATTCCTGACAAAGGAGCA	1332
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Qy	1321	GGTTACCCCTTCGGATTTTACGGTGATTACTACGGGTATACCAACTCATGTGTTCTTTCG	1380
Db	1331	GGTTACCCCTTCGGATTTTACGGTGATTACTACGGGTATACCAACTCATGTGTTCTTTCG	1390
Qy	1381	ATGAATCTAAATTTGATCCACTTCTCGAGGACGTCAAACGTATGCTTACGAAACCAA	1440
Db	1391	ATGAATCTAAATTTGATCCACTTCTCGAGGACGTCAAACGTATGCTTACGAAACCAA	1450
Qy	1441	CATGATTAATTTGATCATCATGATATTATGCGCTGGAGAGAGAAAGGGGACAGCTCCAC	1500
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Qy	1501	CCAAATTCAGAGACTTGCACATATTATGTCGATGGGCGAGGGGGGTATATAATGATGAT	1560
Db	1511	CCAAATTCAGAGACTTGCACATATTATGTCGATGGGCGAGGGGGGTATATAATGATGAT	1570
Qy	1561	GTCGGGAAAACATAAAGCTGGCCAAAGTATGAGAGATATCACCGGAAATAGTCTGGTAC	1620
Db	1571	GTCGGGAAAACATAAAGCTGGCCAAAGTATGAGAGATATCACCGGAAATAGTCTGGTAC	1630
Qy	1621	GTCACCATTAATGACAGATGTTTGGGGAAATTTCACTGTAAACGAGAGGGGACGTTCCGTT	1680
Db	1631	GTCACCATTAATGACAGATGTTTGGGGAAATTTCACTGTAAACGAGAGGGGACGTTCCGTT	1690
Qy	1681	TGGGTGAAGCATATAATAGGAACCAAGAGCGGAAAAATTAATCTTCTCATGACAGAGCTT	1740
Db	1691	TGGGTGAAGCATATAATAGGAACCAAGAGCGGAAAAATTAATCTTCTCATGACAGAGCTT	1750
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Db	1751	CCGATCACTCATACACCCCAATATAATTTGGAAGCTT	1786
RESULT 5			
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LOCUS		1786 bp	DNA
DEFINITION	Alpha-amy-lase with high productivity.		linear
ACCESSION	BD144003		
VERSION	BD144003.1	GI:27849761	
KEYWORDS	JP 2002112792-A/1.		
SOURCE	Bacillus sp. KSM-AP1378		
ORGANISM	Bacillus sp. KSM-AP1378		
REFERENCE	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
AUTHORS	1 (bases 1 to 1786)		
	Araki,H., Endo,K., Hagiwara,H., Igarashi,K., Hayashi,Y. and		
	Ozaki,K.		
	Alpha-amy-lase with high productivity		
	Patent: JP 2002112792-A 1 16-APR-2002;		
TITLE	Alpha-amy-lase with high productivity		
JOURNAL	Patent: JP 2002112792-A 1		
COMMENT	OS	Bacillus sp. KSM-AP1378	
	PN	JP 2002112792-A/1	
	PD	16-APR-2002	
	PF	11-OCT-2000 JP 2000310605	
	PI	HIROFUKI ARAKI,KEIJI ENDO,HIROSHI HAGIWARA,KAZUAKI IGARASHI,	
	PI	YASUHIRO HAYASHI,KATSUYA OZAKI	
	PC	C12N15/09, C11D3/386, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N9/	
	PC	28//	
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	PC	C12N15/00,	
	PC	C12N5/00, (C12N15/00, C12R1:07)	
	CC	Alpha-amy-lase with high productivity	
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	Match	1776;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	
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Db	11	ATATTAATTGGAATGAATAACCTATGTAAAAATATGTAGCGATTTGCCGACAGAAAAAAC	70								
Oy	61	TTCGGAGTTAGGAAGTGAATATTAAGAATTTTTTTTGACTTTGTGTGAAAAACGTTGCAT	120								
Db	71	TTCGGAGTTAGGAAGTGAATATTAAGAATTTTTTTTGACTTTGTGTGAAAAACGTTGCAT	130								
Oy	121	AAATTTGAAGGAGAGCGGCTTTTATATGAACCTCAATAACGGTAAATTTAGCGTACTATTA	180								
Db	131	AAATTTGAAGGAGAGCGGCTTTTATATGAACCTCATACCGTATATTAAGCGTACTATTA	190								
Oy	181	AACATATTTTGTAGCTGTAGCTGTTTTGTTTCCATATATGA CGGAACGACAAGCCCAT	240								
Db	191	ACACTATTTGTAGCTGTAGCTGTTTTGTTTCCATATATGA CGGAACGACAAGCCCAT	250								
Oy	241	CATATATGGAGCAATGGGACCATGATCAGTATTTTGAAATGSCATTTGCCAATATGACGG	300								
Db	251	CATATATGGAGCAATGGGACCATGATCAGTATTTTGAAATGSCATTTGCCAATATGACGG	310								
Oy	301	AACACACTGGAAACAGGTTACGATGACGACGACGCTAACTTAAAGATTAAGGAAATTCACGCT	360								
Db	311	AACACACTGGAAACAGGTTACGATGACGACGACGCTAACTTAAAGATTAAGGAAATTCACGCT	370								
Oy	361	GTITTGATTTCTCTCGCATGGAAGGGGACTTCGCAAAATGATGTTGGGTAATGTGCTCAT	420								
Db	371	GTITTGATTTCTCTCGCATGGAAGGGGACTTCGCAAAATGATGTTGGGTAATGTGCTCAT	430								
Oy	421	GATTTGTAACGATCTTGTGTAGTTTAACCAAAGGGAA CCGTCCGTAACAAATATGAGACA	480								
Db	431	GATTTGTAACGATCTTGTGTAGTTTAACCAAAGGGAA CCGTCCGTAACAAATATGAGACA	490								
Oy	481	AGGAGTCAGTTGGCAAGGCGCGTAGCACTCTTTGAAAATTAACGGGATTTCAAGTTATGGG	540								
Db	491	AGGAGTCAGTTGGCAAGGCGCGTAGCACTTTGAAAATTAACGGGATTTCAAGTTATGGG	550								
Oy	541	GANTGCTGTATGAATCATTAAGGAGGACAGACGGGACAGAGATGTTAAATTCGGTGGAA	600								
Db	551	GANTGCTGTATGAATCATTAAGGAGGAGGACAGACGGGACAGAGATGTTAAATTCGGTGGAA	610								
Oy	601	GTGAACCGAAGCAACCGAACCAGAAATATCACGGTAATATACATTGAAGCATGGACG	660								
Db	611	GTGAACCGAAGCAACCGAACCAGAAATATCACGGTAATATACATTGAAGCATGGACG	670								
Oy	661	AAATTTGATTTCCCTGGAGAGGAAATATACCATTCCAATTAAATGCGCTGGTATCAT	720								
Db	671	AAATTTGATTTCCCTGGAGAGGAAATATACCATTCCAATTAAATGCGCTGGTATCAT	730								
Oy	721	TTTGATGAGGACAGATGGGATCACTGACGCTGACGCTTCAAGCAAAATATATTAATTGACA	780								
Db	731	TTTGATGAGGACAGATGGGATCACTGACGCTGACGCTTCAAGCAAAATATATTAATTGACA	790								
Oy	781	GGTACCGGAAAGGATGGGACTGGGAGTGAATATTAAGAAACGGCAACTATGATTAACCTT	840								
Db	791	GGTACCGGAAAGGATGGGACTGGGAGTGAATATTAAGAAACGGCAACTATGATTAACCTT	850								
Oy	841	ATGTATGACAGCATTTGATATGATATCATCCAGAAATATCATGAACTTAAAGATTTGGGGA	900								
Db	851	ATGTATGACAGCATTTGATATGATATCATCCAGAAATATCATGAACTTAAAGATTTGGGGA	910								
Oy	901	GTITTGATATCAAAATACATTAATCTAGATGATTTTGAATGATGCTGTGAAA CATATT	960								
Db	911	GTITTGATATCAAAATACATTAATCTAGATGATTTTGAATGATGCTGTGAAA CATATT	970								
Oy	961	AAATACAGCTATACAGAGATTTGGCTTAACATGTGGTAAACACCAAGGTAAACCATG	1020								

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PI	KATSUYA OKAI
PC	C12N15/09, C1D3/386, C12N1/15, C12N1/19, C12N1/21, C12N5/10, PC
PC	C12N9/26//
PC	(C12N15/09, C12R1:125), (C12N1/21, C12R1:125), (C12N9/26, PC
CC	C12R1:125), C12N15/00,
CC	C12N5/00, (C12N15/00, C12R1:125)
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FT	source
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Best Local Similarity	100.0%; Pred. No. 0;
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DB	71 TTGGAGGTGGAAGTAGATTAATAAGAATTTTCTGCTGTTGTAAGAAACGCTTGCAAT 130
OY	121 AAATGGAAGAGAGGGTCTTTTATGAAAATTTCATACCGTAATTAATTAGCGTACTATTA 180
DB	131 AAAATGGAAGAGAGGGTCTTTTATGAAAATTTCATACCGTAAATTAATTAGCGTACTATTA 190
OY	181 ACACTATTGTTAGCTGTAGCTGTTTTGTTTCATATATGACGNAACGACAAGCCCAT 240
DB	191 ACACATATTGTTAGCTGTAGCTGTTTTGTTTCATATATGACGNAACGACAAGCCCAT 250
OY	241 CATATATGGAGCAATGGAGCACATGATTCAGATTTTGAATGGCAATTTGCCAATGACGGG 300
DB	251 CATATATGGAGCAATGGAGCACATGATTCAGATTTTGAATGGCAATTTGCCAATGACGGG 310
OY	301 AACACATGGAACAGAGTTACGAGATGAGAGCGCTAACCTTAAGAAGTAAGGATTAACGGCT 360
DB	311 AACACATGGAACAGAGTTACGAGATGAGAGCGCTAACCTTAAGAAGTAAGGATTAACGGCT 370
OY	361 GTTTGATTTCCCTCGATGGAAGGGGACTTCGCAAAATGATGTTGGGTATGGTGCTAT 420
DB	371 GTTTGATTTCCCTCGATGGAAGGGGACTTCGCAAAATGATGTTGGGTATGGTGCTAT 430

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QY 781 GGTACCGGAAAGGATGGGACTGGGAGTATAGATATAGAGAACCGCACTATGATTAACCTT 840
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Db 911 GTTGGATATCAATACACTATCTATGATGATGATTAAGATGATGATGATGATGATGATGAT 970
QY 961 AATATAGCATATACGAGAGATTTGGCTTAAACATATGCTGATTAACCAAGTAAACCAATG 1020
Db 971 AATATAGCATATACGAGAGATTTGGCTTAAACATATGCTGATTAACCAAGTAAACCAATG 1030
QY 1021 TTTGAGTTGCAAGATTTTGGAAAAATGACCTTGTCTGCAATGCAAAATCTTTAAATTA 1080
Db 1031 TTTGAGTTGCAAGATTTTGGAAAAATGACCTTGTCTGCAATGCAAAATCTTTAAATTA 1090
QY 1081 ACAAGTTGGAATCACTCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
Db 1091 ACAAGTTGGAATCACTCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1150
QY 1141 AATAGTGTGGCTATTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
Db 1151 AATAGTGTGGCTATTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1210
QY 1201 CCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
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QY 1321 GGTATACCTTCCGATATTTACGGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
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QY 1381 ATGAAATCTAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
Db 1391 ATGAAATCTAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1450
QY 1441 CATGATTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
Db 1451 CATGATTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1510
QY 1501 CCAAAATTCAGAGCTTTCAGACTATTTATGTCGATGAGGCGAGGGGTTAAATGATGAT 1560
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QY 1621 GTACACATTAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
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QY 1681 TGGGTGAAGCAATTAATTAAGGAGCAAGAGGGAATTAATTAATTAATTAATTAATTAAT 1740
Db 1691 TGGGTGAAGCAATTAATTAAGGAGCAAGAGGGAATTAATTAATTAATTAATTAATTAAT 1750
QY 1741 CCGATCACTCATACACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1776
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RESULT 7
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LOCUS AR541695
DEFINITION Sequence 1 from patent US 6743616.
ACCESSION AR541695
VERSION AR541695.1 GI:53933768
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 1786)
AUTHORS Araki, H., Endo, K., Hagihara, H., Igarashi, K., Hayashi, Y. and Ozaki, K.
TITLE Highly productive alpha-amylases
JOURNAL Patent: US 6743616-A 1 01-JUN-2004;
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ORIGIN

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Query Match 100.0%; Score 1776; DB 6; Length 1786;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 1776; Conservative 0;

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Db 11 ATATTAATTTGAAATGAACACCTATGAAATATGATGATGATGATGATGATGATGATGATGAT 70
QY 61 TTTGGAGTTTGAAGATGATTAATTAAGATTTTGTGATGATGATGATGATGATGATGATGAT 120
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QY 121 AATTTGAAGAGAGGGGCTTTTATGAAACTTCAATACCGTATATAGCTACTATTA 180
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Db 191 ACACTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 250
QY 241 CATATGGAACGATATGGAACCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
Db 251 CATATGGAACGATATGGAACCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 310
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LOCUS
DEFINITION Sequence 3 from Patent EP1199356.
ACCESSION AX428291
VERSION AX428291.1 GI:21538247
KEYWORDS
SOURCE
ORGANISM Bacillus sp. KSM-AP1378
Bacillus sp. KSM-AP1378
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
REFERENCE
1 Areki, H. C., Hagihara, H. C., Hayashi, Y. C., Endo, K. C., Igarashi, K. C.
and Ozaki, K. C.
TITLE Highly productive alpha-amylases
JOURNAL Patent: EP 1199356-A 3 24-Apr-2002;
Kao Corporation (JP)
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RESULT 9

AX601433/c AX601433 6661 bp DNA linear PAT 17-FEB-2003
DEFINITION Sequence 3 from Patent WO02092741.
ACCESSION AX601433
VERSION AX601433.1 GI:28401480
KEYWORDS

SOURCE

ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE

AUTHORS
TITLE
JOURNAL
1
EskeJund,M.B., Schuelein,M., Nielsen,V.S. and Smets,J.
Detergent compositions comprising Bacillus subtilis subtilis peptate lyases
Patent: WO 02092741-A 3 21-NOV-2002;
Novozymes A/S (DK)
Location/Qualifiers

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 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1458)
 AUTHORS Svendsen,A., Blag.,ang.-rd.-Frantzen,H. and Borchert,T.Vedel.
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RESULT 12
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 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1455)
 AUTHORS Ouchtrud, H., Biss, ang, rd-Frantzen, H., stergaard, P., Rahbek, .,
 Rasmussen, M., Dolberg, and Van Der Zee, P.
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 DB 1441 GCTATGAATCTAAATATGAGACCTCTTCTGACAGGACGTCGAACTTTGCTATGATGACG 1200

DB 61 GGAATCATTTGGAACAGGTTGAGGATGACGACGATTAATTAAAGATTAAGGATTAACA 120
 QY 358 GCTTTTGAATTCCTCTGATGGAAGGAGGACTTGGCAATATGATGTTGGTATGAGGCC 417
 DB 121 GCTATGATGATCCCACTGATGGAAGGAGGACTTCCGAAATGATGATGATGAGGCC 180
 QY 418 TATGATTTGATGATCTTTGATGATTTTAAACCAAAAGGAAACCGTCCGTACAAAATATG 477
 DB 181 TATGATTTTATGATCTTTGATGATTTTAAACCAAGAGGAGCGGTTGTACAAAATATG 240
 QY 478 ACAAGAGTCAAGTTGCAAGTCCCGTGAATCTTTTGAATAATACGGGATTTCAAGTTAT 537
 DB 241 ACAAGAGTCAAGTTGCAAGTCCCGTGAATCTTTTGAATAATACGGGATTTCAAGTTAT 300
 QY 538 GGGATGTCGTGATGATTAAGTGAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGG 597
 DB 301 GGTATGTCGTGATGATTAAGTGAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
 QY 598 GAAGTGAACCGAAGCAACCGAAGCAAGAAATATCAAGTGAATTAACCATTTGAAGCATG 657
 DB 361 GAAGTGAATCGAAGCAACCGAAGCAAGAAATATCAAGTGAATTAACCATTTGAAGCATG 420
 QY 658 ACAAGATTTGATTTCCCTGGAAGGAAATACCATTCGAACTTTAAATGGCGCTGAT 717
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 QY 718 CATTTGATGGAAGATTTGGATGATGATGATGATGATGATGATGATGATGATG 777
 DB 481 CATTTGATGGAAGATTTGGATGATGATGATGATGATGATGATGATGATGATG 540
 QY 778 AGAGTACCGGAAGAGGATGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 837
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 QY 838 CTATGATGACAGCATTTGATGATGATGATGATGATGATGATGATGATGATG 897
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 QY 898 GGAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 957
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 DB 781 ATGTTGACAGTGGAGATTTTGAAGAAATGACCTTGCATATGCAATGCAAACTATTTAAT 840
 QY 1078 AAAACAAGTTGGAATCACTCCGTTGATGATGATGATGATGATGATGATGATG 1137
 DB 841 AAAACAAGTTGGAATCACTCCGTTGATGATGATGATGATGATGATGATGATG 900
 QY 1138 TCTAATAGTGGCTATTTTATATGAGAAATATTTAAATGGTCTGCTGCAAAA 1197
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 QY 1198 CACCTATACATGAGTCACTTTGTTATGATACCATGACTCTGACGAGAGAGATG 1257
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 QY 1318 CAAGTTACCTGCTGATTTTAAAGTATGATGATGATGATGATGATGATGATG 1377
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QY 1618 ACCGTACCATTAATGATGATGGTGGGGAATTTCACTGTAAACGAGAGGAGGAGTTTG 1677
DB 1381 ACCGTACCATTAATGATGATGGGGAATTTCACTGTGTATTTCTGTATTAAGAGGAGCTTGG 1440
QY 1678 GTTGGGTGAAGCAA 1692
DB 1441 GTTGGGTGAAGCAA 1455

RESULT 13
AR049517 1455 bp DNA linear PAT 29-SEP-1999
LOCUS AR049517
DEFINITION Sequence 4 from patent US 5824531.
ACCESSION AR049517
VERSION AR049517.1 GI:6005556
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1455)
AUTHORS Outtup,H., Bleg.ang.-rd-Frantzen,H., stergaard,P.Rahbek.,
Rasmussen,M.Dolberg, and Van der Zee,P.
TITLE Alkaline bacillus amyase
JOURNAL Patent: US 5824531-A 4 20-OCT-1998;
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source 1. 1455
/organism="Unknown"
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Query Match 65.7%; Score 1167; DB 6; Length 1455;
Best Local Similarity 87.6%; Pred. No. 1 2e-262;
Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

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QY 298 GGAAGAACCTGGAACAGGTGAACGATGACGAGCTTAACCTTAAGATTAAGGATTAAC 357
DB 61 GGAAGAACCTGGAACAGGTGAACGATGACGAGCTTAACCTTAAGATTAAGGATTAAC 120
QY 358 GCTGTTGGAATTCCTCTGATGGAAGGGAATTCGCCAAATGATGTTGGTATGTCGC 417
DB 121 GCTGTTGGAATTCCTCTGATGGAAGGGAATTCGCCAAATGATGTTGGTATGTCGC 180
QY 418 TATGATTTGATGATCTTGTGATGTTAAACAAAGAGGAACCGTCCGTACAAATATGCG 477
DB 181 TATGATTTGATGATCTTGTGATGTTAAACAAAGAGGAGCGTTCGTACAAATATGGA 240
QY 478 ACAAGAGATCAGTTCGAAGGTGCGGTGACATCTTTGAAATTAACGGGATTCAGTTAT 537
DB 241 ACAAGAGATCAGTTCGAAGGTGCGGTGACATCTTTGAAATTAACGGGATTCAGTTAT 300
QY 538 GGGGATGTCGTGATGATCATTAAGGTGAGAGAGGAGCAGAGATGTAATGCGGTG 597
DB 301 GGGGATGTCGTGATGATCATTAAGGTGAGAGAGGAGCAGAGATGTAATGCGGTG 360
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DB 1441 GTTGGGTGAAGCAA 1455

DB 361 GAAGTGAATCGAGCAACCGAAACAGAGAAACCTCAGAGATATGCAATAGAACGCTG 420
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DB 481 CATTTGATGGAACAGATTTGGGATCAGTCAGCTTACAGTTCAGAAACAAATATATAATTC 540
QY 778 AGAGGTAACCGAAGGATGGAACCTGGGAAGTATATGAGAAAGGCACTATGATTC 837
DB 541 AGAGGTAACCGAAGGATGGAACCTGGGAAGTATATGAGAAAGGCACTATGATTC 600
QY 838 CTATGATGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 897
DB 601 CTATGATGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
QY 898 GGAGTTGGTATACAAATACCTTAATCTAGATGATGATGATGATGATGATGATGATGAT 957
DB 661 GGAGTTGGTATACAAATACCTTAATCTAGATGATGATGATGATGATGATGATGATGATG 720
QY 958 ATTAATATACGATATACGAGATTTGGCTTAACATATGTCGTAACCAAGGTAAACA 1017
DB 721 ATTAATATATAGCTTTACGAGATTTGGCTTAACATATGTCGTAACCAAGGTAAACA 780
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DB 781 ATGTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
QY 1078 AAAACAGTTGGATACACTCCGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1137
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QY 1198 CACCCATATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1257
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DB 1381 ACCGTACCATTAATGATGATGGGGAATTTCACTGTGTATTTCTGTATTAAGAGGAGCTTGG 1440
QY 1678 GTTGGGTGAAGCAA 1692
DB 1441 GTTGGGTGAAGCAA 1455

RESULT 14
ARI04348
LOCUS ARI04348 1455 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 4 from patent US 6093562.
ACCESSION ARI04348
VERSION ARI04348.1 GI:12817056
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1455)
AUTHORS Bisg ang rd-Frantzen,H., Svendsen,A. and Borchert,T.Vedel.
TITLSE Amylase variants
JOURNAL Patent: US 6093562-A 4 25-JUL-2000;
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source location/Qualifiers
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Query Match 65.7%; Score 1167; DB 6; Length 1455;
Best Local Similarity 87.6%; Pred.No.1.2e-262;
Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0;
QY 238 CATCATATGGAAGCAATGGAACCATGATGCAATTTTGAATGGCATTTGCCAAATGAC 297
DB 1 CATCATATGGAACAAATGCTACTATGATGCAATATTTTCGATGATTTTCCCAAATGAC 60
QY 298 GGGAACTGGAACAGGTTACGAGATGACGACACTAATTAAGAGTAAGGATTTACC 357
DB 61 GGGATATGGAACAGGTTAGGATGACGACACTAATTAAGAGTAAGGATTTACC 120
QY 358 GCTGTTGATTCCTCTGATGAGAGGAGCTTCGCAAAATGATGTTGGTATGTCGCC 417
DB 121 GCTGATATGATCCCACTGATGAGAGGAGCTTCGCAATGATGATGTTATGAGGCC 180
QY 418 TATGATTTGATGATCTTTGATGATTTTACCAAAAGGAAACGTCCTGTAACAAATATGAC 477
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QY 658 ACGAAATTTGATTCCTGGAAGAGAAATCCATTCCTTAATGCGCGTGTAT 717
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DB 541 AGGGAACAGGCAAGGCTGGAAGTGGAGATGATCAGAGATGGAATGATGATAT 600
QY 838 CTATATGATGAGCATTTGATGATGATCAGAGTAATCAATGAATCTTAAGAAATGG 897
DB 601 CTATATGATGAGCATTTGATGATGATCAGAGTAATCAATGAATCTTAAGAAATGG 660
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DB 661 GGAATTTGATATACATTAATCTATGATGATGATGATGATGATGATGATGATGAT 720

QY 958 ATTAATACAGCTATACAGAGATTGGCTAACACATGTTGGTATACACACAGTTAAACA 1017
DB 721 ATAAATATAGCTTTAGAGAGATTGGCTTACACATGTTGGTATACACACAGTTAAACA 780
QY 1018 ATGTTTCAGTTGAGATATTTGGAAAAATGACCTTCCTGCAATCGAAATCTATTTAAT 1077
DB 781 ATGTTTCAGTTGAGATATTTGGAAAAATGACCTTCCTGCAATCGAAATCTATTTAAT 840
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QY 1378 TCGATGAATCTAAATTTGATCCACTCTGCAAGGAGTCAAAACGTTATGCTTACGAAAC 1437
DB 1141 GCTATGAATCTAAATTTGATCCACTCTGCAAGGAGTCAAAACGTTATGCTTACGAAAC 1200
QY 1438 CAACATGATTTATTTGATCATGATATTTATGCTGAGCAGAGAGAGGAGCAGCTCC 1497
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QY 1498 CACCAATTTCAAGACTTGAATTTATGTCGATGAGGCGGAGGATTAATTAATGATG 1557
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DB 1381 ACCGTCACTTAATGAGATGTTGGGGAATTTCTCTGTAATGAGAGGCTCGTTCC 1440
QY 1678 GTTTGGGTGAAGCA 1692
DB 1441 GTTTGGGTGAAGCA 1455
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ARI29912
LOCUS ARI29912 1455 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 9 from patent US 6187576.
ACCESSION ARI29912
VERSION ARI29912.1 GI:14117809
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1455)
AUTHORS Svendsen,A., Borchert,T.Vedel. and Bisg ang rd-Frantzen,H.
TITLSE alpha-amylase mutants
JOURNAL Patent: US 6187576-A 9 13-FEB-2001;
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source location/Qualifiers
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ORIGIN

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 2, 2005, 17:25:37 ; Search time 670 Seconds
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Title: US-08-952-741-1
Perfect score: 1776
Sequence: 1 atataatctgaaatgacac.....ccaataaactggaagctt 1776

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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2: geneseqn1990s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1776	100.0	1776 2	AAT51339 Coding se
2	1776	100.0	1776 6	AAD44364 Bacillus
3	1776	100.0	1786 3	AAC66234 Mutant al
4	1776	100.0	1786 6	AAK99881 DNA of Ba
5	1187.2	66.8	6661 10	AAD49392 pMO1995 P
6	1167	65.7	1455 2	AAT00776 Bacillus
7	1167	65.7	1455 2	AAK59636 DNA encod
8	1167	65.7	1455 2	AAK59632 DNA encod
9	1167	65.7	1455 2	AAK57597 wild type
10	1167	65.7	1455 3	AAA48480 Bacillus
11	1167	65.7	1455 3	AAA48485 Bacillus
12	1167	65.7	1455 6	ABL50564 Bacillus
13	1167	65.7	1455 6	AAK20022 Bacillus
14	1167	65.7	1455 6	AAI72211 Bacillus
15	1167	65.7	1455 6	ABL96207 Termany1-
16	1167	65.7	1455 10	ADJ92077 Termany1-
17	1157.4	65.2	1455 2	AAK57592 wild type
18	961	54.1	1551 6	ABL41241 Bacillus
19	945	53.2	5793 6	AAK17998 Plasmid P
20	945	53.2	5943 6	AAK17997 Plasmid P

21	944.2	53.2	2086 4	AAD16804	AAD16804 Bacillus
22	944.2	53.2	2086 4	AAD16803	AAD16803 Bacillus
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24	941.2	53.0	1458 3	AAA30783	AAA30783 DNA encod
25	941.2	53.0	1458 5	AAK63114	AAK63114 Bacillus
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27	941.2	53.0	1458 6	AAK20027	AAK20027 Bacillus
28	941.2	53.0	1458 6	AAI72216	AAI72216 Bacillus
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30	941.2	53.0	1458 10	ADJ92087	ADJ92087 Termany1-
31	933.6	52.6	2341 4	AAD16805	AAD16805 Bacillus
32	932	52.5	2330 4	AAD16808	AAD16808 Bacillus
33	927	52.2	1455 2	AAK59637	AAK59637 DNA encod
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ALIGNMENTS

RESULT 1	
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ID AAT51339 standard; DNA; 1776 BP.	
XX	
AC AAT51339;	
XX	
DT 17-OCT-2003 (revised)	
DT 27-AUG-2003 (revised)	
DT 11-NOV-1997 (first entry)	
XX	
DE Coding sequence for alkaline liquefying alpha-amylase.	
XX	
KW Alkaline liquefying alpha-amylase; Bacillus; alpha-amylase; detergent;	
KW starch-related polysaccharide; hydrolysis; enzyme; surfactant resistance;	
KW alpha-1,4-glucosidic link; alkalophilic Bacillus; laundry detergent;	
XX	
OS Bacillus sp; KSM-AP1378.	
XX	
EH Key	Location/Qualifiers
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XX	
PN W09700324-A1.	
XX	
PD 03-JAN-1997.	
XX	
PF 14-JUN-1996; 96MO-JP001641.	
XX	
PR 14-JUN-1995; 95JP-00147257.	
XX	
PA (KAOS) KAO CORP.	
XX	
PI Hatada Y, Ozaki K, Ara K, Kawai S, Ito S;	
DR WPI: 1997-118708/11.	
XX	
DR P-PSDB; AAM11326.	
XX	
PT DNA encoding alkaline liquefying alpha-amylase - useful in dish-washing	
XX	
PS Claim 8; Page 23-26; 40pp; English.	

XX This sequence represents the coding sequence for an alkaline liquefying
 CC alpha-amylase. Alpha-amylase is an enzyme that acts on starch-related
 CC polysaccharides, hydrolyzing the alpha-1,4-glucoside bond of the
 CC polysaccharide molecule. Alkaline liquefying alpha-amylases exhibit
 CC resistance to surfactants used in detergents, and decompose starch or
 CC starch-related polysaccharides in a highly random manner. The Bacillus
 CC species KSM-AP1378, from which this sequence was isolated, is an
 CC alkalophilic Bacillus strain. It was isolated from soil in the vicinity
 CC of the city of Tochi. The enzyme is useful in improving the efficiency
 CC of dish-washing and laundry detergents, particularly on starch dirt.
 CC (Updated on 27-AUG-2003 to correct OS field.) (Updated on 17-OCT-2003 to
 CC standardise OS field)

XX Sequence 1776 BP; 575 A; 305 C; 417 G; 479 T; 0 U; 0 Other;

Query Match 100.0%; Score 1776; DB 2; Length 1776;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1776; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATATTAATTTGAATGACCTTATGAAATATGTCGATTCGCGACGAGAAAAAC 60
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 DB 61 TTGGAGTTAGAGATGATTAAGGATTTTGGACTGTGTGAAACGCTTGCAAT 120
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 DB 121 AATTTGAGAGAGAGGCTTTTATGAACTTCATACCGTAATTAATTCGTAATTA 180
 QY 181 ACCTATTTGACTGATGCTGTTTGTTCATATATGACGAGACGACAGCCCAT 240
 DB 181 ACCTATTTGACTGATGCTGTTTGTTCATATATGACGAGACGACAGCCCAT 240
 QY 241 CATATGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
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 DB 541 GATGTCGATGATGATTAAGGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
 QY 601 GTGACCGAGAGCAACGAAACCAAGAAATATCAGTGAATACCATTTGAAGCAT 660
 DB 601 GTGACCGAGAGCAACGAAACCAAGAAATATCAGTGAATACCATTTGAAGCAT 660
 QY 661 AAATTTGATTTCTCTGGAAGAGAAATACCATTTGAAGCATTTAATGAGCTG 720
 DB 661 AAATTTGATTTCTCTGGAAGAGAAATACCATTTGAAGCATTTAATGAGCTG 720
 QY 721 TTGATGAGGAGCAATTTGAGATCACTGACGCTTCAAGCAAAATATTAATCA 780
 DB 721 TTGATGAGGAGCAATTTGAGATCACTGACGCTTCAAGCAAAATATTAATCA 780
 QY 781 GGTACCGGAAAGGATGAGCTGAGAAATGATATAGAAACGCAATATGATTA 840

DB 781 GGTACCGGAAAGGATGAGCTGAGAAATGATATAGAAAGGCAACTATGATTA 840
 QY 841 ATGATGACGACATTTGATGATCACTGACGCTTCAAGCAAAATATTAATCA 900
 DB 841 ATGATGACGACATTTGATGATCACTGACGCTTCAAGCAAAATATTAATCA 900
 QY 901 GTTTGATTTCTCTGGAAGAGAAATACCATTTGAAGCATTTAATGAGCTG 960
 DB 901 GTTTGATTTCTCTGGAAGAGAAATACCATTTGAAGCATTTAATGAGCTG 960
 QY 961 AAATTTGATTTCTCTGGAAGAGAAATACCATTTGAAGCATTTAATGAGCTG 1020
 DB 961 AAATTTGATTTCTCTGGAAGAGAAATACCATTTGAAGCATTTAATGAGCTG 1020
 QY 1021 TTGACGTTGCAAGATTTTGAAGAAATGACCTTGTGCAATGAAACCTATTA 1080
 DB 1021 TTGACGTTGCAAGATTTTGAAGAAATGACCTTGTGCAATGAAACCTATTA 1080
 QY 1081 ACAAGTTGAAATCACTCGGTTCGATGTTCCCTTCAATTAATTTGTAATGAT 1140
 DB 1081 ACAAGTTGAAATCACTCGGTTCGATGTTCCCTTCAATTAATTTGTAATGAT 1140
 QY 1141 AATAGTGTGCTATTTGATATGAGAAATATTTAAATGATGTTCTGTCAAAAAC 1200
 DB 1141 AATAGTGTGCTATTTGATATGAGAAATATTTAAATGATGTTCTGTCAAAAAC 1200
 QY 1201 CCTATATGACGATCACTTTGTTGTAATCACTGACTCTACGACGAGAGACATT 1260
 DB 1201 CCTATATGACGATCACTTTGTTGTAATCACTGACTCTACGACGAGAGACATT 1260
 QY 1261 TCCTTTGTCATTCGAGGTTCAACCACTGAGATGATGATGATTTCTGCAAGAG 1320
 DB 1261 TCCTTTGTCATTCGAGGTTCAACCACTGAGATGATGATGATTTCTGCAAGAG 1320
 QY 1321 GGTACCTTCCGATATTTACGAGTATTAACCTGATACCAATCATGTTCTT 1380
 DB 1321 GGTACCTTCCGATATTTACGAGTATTAACCTGATACCAATCATGTTCTT 1380
 QY 1381 ATGAAATCTTAAATTTGATCACTTTCGAGGAGGAGGAGGAGGAGGAGGAG 1440
 DB 1381 ATGAAATCTTAAATTTGATCACTTTCGAGGAGGAGGAGGAGGAGGAGGAG 1440
 QY 1441 CATGATTTATTTGATCATATGATATTTATGCGCTGAGAGAGAGGAGGAGG 1500
 DB 1441 CATGATTTATTTGATCATATGATATTTATGCGCTGAGAGAGAGGAGGAGG 1500
 QY 1501 CCATTTTCAAGACTTGCATATTTATGTCGATGAGGAGGAGGAGGAGGAGGAG 1560
 DB 1501 CCATTTTCAAGACTTGCATATTTATGTCGATGAGGAGGAGGAGGAGGAGGAG 1560
 QY 1561 GTGCGGAAACATTAAGCTGCGCAAGATGAGAGATATCAACGGAATGATGAT 1620
 DB 1561 GTGCGGAAACATTAAGCTGCGCAAGATGAGAGATATCAACGGAATGATGAT 1620
 QY 1621 GTGACCATTAATGAGAGATGTTGAGGAGGAGGAGGAGGAGGAGGAGGAG 1680
 DB 1621 GTGACCATTAATGAGAGATGTTGAGGAGGAGGAGGAGGAGGAGGAGGAG 1680
 QY 1681 TGGGTAAACCAATTAATTAAGAAACAAAGAGGCAAAATATCTTCTCAATG 1740
 DB 1681 TGGGTAAACCAATTAATTAAGAAACAAAGAGGCAAAATATCTTCTCAATG 1740
 QY 1741 CCGATCATCTATACCCCAATTAATTTGGAAGCTT 1776
 DB 1741 CCGATCATCTATACCCCAATTAATTTGGAAGCTT 1776

RESULT 2
 AAD4364
 ID AAD4364 standard; DNA; 1776 BP.
 XX
 AC AAD4364;

[illegible]

QY	12	AAATGGAAGAGAGGGGCTTTTATGAAACCTCATACCGTAAATTAAGGTCATTA	180
Db	121	AAATTTGAAGAGAGGGTCTTTTATGAAACTTATACCGTAAATTAAGGTCATTA	180
QY	181	ACACTATTTGTAGCTGTAGCTGTCTTTGTTCATATATGACGGAAACGACACAGCCCAT	240
Db	181	ACACTATTTGTAGCTGTAGCTGTCTTTGTTCATATATGACGGAAACGACAGCCCAT	240
QY	241	CATATATGGGACGAATGGGACCATGATGCAGATTTTGAATGGCAATTTGCCAAATGACGGG	300
Db	241	CATATATGGGACGAATGGGACCATGATGCAGATTTTGAATGGCAATTTGCCAAATGACGGG	300
QY	301	AACCACTGGGAAACAGTTTACGAGATGACGACGCTTACTTAAAGAGTAAAGGATTAACGGCT	360
Db	301	AACCACTGGGAAACAGTTTACGAGATGACGACGCTTACTTAAAGAGTAAAGGATTAACGGCT	360
QY	361	GTTTGGAATTCCTCCCTGATGGAGGGGACTTCGCAAAATGATGTGGGTATGGTGCCTAT	420
Db	361	GTTTGGAATTCCTCCCTGATGGAGGGGACTTCGCAAAATGATGTGGGTATGGTGCCTAT	420
QY	421	GATTGTGACGATCTTGTGTGAGTTTAAACCAAAAGGAAAACCGTCCGTACAAAATATGCGACA	480
Db	421	GATTGTGACGATCTTGTGTGAGTTTAAACCAAAAGGAAAACCGTCCGTACAAAATATGCGACA	480
QY	481	AGGAGTCAGTTTGCAGAGGTCGCCGTACATCTTTGAAAAATTAACGGGATTTCAAGTTTATGGG	540
Db	481	AGGAGTCAGTTTGCAGAGGTCGCCGTACATCTTTGAAAAATTAACGGGATTTCAAGTTTATGGG	540
QY	541	GATGTCGATGATCATTAAGGTGAGACGACGAGACGAGATGATTAATGCGGTGGAA	600
Db	541	GATGTCGATGATCATTAAGGTGAGACGAGACGAGATGATTAATGCGGTGGAA	600
QY	601	GTGAACCGAAGCAACCGAAACCAAGAAATATCAAGTGAATACCAATTTGAAGCATGGAACG	660
Db	601	GTGAACCGAAGCAACCGAAACCAAGAAATATCAAGTGAATACCAATTTGAAGCATGGAACG	660
QY	661	AAATTTGATTTCCCTCGAAGAGGAAATACCATTCCAACTTTAAATGGCCGTGATCAT	720
Db	661	AAATTTGATTTCCCTCGAAGAGGAAATACCATTCCAACTTTAAATGGCCGTGATCAT	720
QY	721	TTTGATGGGACAGATTTGGGATCAGTCAAGTCAAGCTTCAGAAACAAATATATTAATTCAGA	780
Db	721	TTTGATGGGACAGATTTGGGATCAGTCAAGTCAAGCTTCAGAAACAAATATATTAATTCAGA	780
QY	781	GGTACCGGAAAGGATGGGACTGGGAAGTATATGAGGAAACGGCAACTATGATTAACCTT	840
Db	781	GGTACCGGAAAGGATGGGACTGGGAAGTATATGAGGAAACGGCAACTATGATTAACCTT	840
QY	841	ATGTATGCAGACATTGATATATGATCATCCAGAGTAATCAATGAACTTGAAAAATGGGGA	900
Db	841	ATGTATGCAGACATTGATATATGATCATCCAGAGTAATCAATGAACTTGAAAAATGGGGA	900
QY	901	GTTTGGTATTAACAAATTAACCTTAATCTAGATGAGATTTGAATCAATGATCTGTGAACAATTT	960
Db	901	GTTTGGTATTAACAAATTAACCTTAATCTAGATGAGATTTGAATCAATGATCTGTGAACAATTT	960
QY	961	AAATACAGCTTACAGAGATTTGGCTAACACATGTGGTAAACCAACAGGTAAACCAATG	1020
Db	961	AAATACAGCTTACAGAGATTTGGCTAACACATGTGGTAAACCAACAGGTAAACCAATG	1020
QY	1021	TTTTCAGTTGCAGAAATTTTGGAAAAATGACCTTGCTGCAATCGAAAACTATTTTAATTA	1080
Db	1021	TTTTCAGTTGCAGAAATTTTGGAAAAATGACCTTGCTGCAATCGAAAACTATTTTAATTA	1080
QY	1081	ACAAAGTTGGAATTCACCTCCGTTCGTGATGTTCTCTTCAATTAATTTTGTAACGATCT	1140
Db	1081	ACAAAGTTGGAATTCACCTCCGTTCGTGATGTTCTCTTCAATTAATTTTGTAACGATCT	1140
QY	1141	AATAGTGGTGCATTTTGTGATATAGAAAAATTTTAATGGTTCGTGTAACAAAAAC	1200
Db	1141	AATAGTGGTGCATTTTGTGATATAGAAAAATTTTAATGGTTCGTGTAACAAAAAC	1200
QY	1201	CCATATACATGACATCTTTGTTGATTAACCATGACTCTGACCGACGAGAAACATTTGAA	1260

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Db 1201 CCTATCATGACGACATCTTGTGATTAACATGACTCTCAGCCAGAGAGCATTTGAA 1260
Qy 1261 TCCCTTGTCATCCGTCGTTCAACCACTGGCATATGATTTGATTCGACAGAGGCA 1320
Db 1261 TCCCTTGTCATCCGTCGTTCAACCACTGGCATATGATTTGATTCGACAGAGGCA 1320
Qy 1321 GGTACCCCTTCGATATTTACGCTGATTAATAAGATTAACAATGATGTTCTTCG 1380
Db 1321 GGTACCCCTTCGATATTTACGCTGATTAATAAGATTAACAATGATGTTCTTCG 1380
Qy 1381 ATGAATCTTAAATTTGATTCATCTTGACGACGTCACAACTGATGCTTACGAA 1440
Db 1381 ATGAATCTTAAATTTGATTCATCTTGACGACGTCACAACTGATGCTTACGAA 1440
Qy 1441 CATGATTTTGTATGATCATGATTAATTCGCTGACGAGAGAGAGGAGCTCCAC 1500
Db 1441 CATGATTTTGTATGATCATGATTAATTCGCTGACGAGAGAGAGGAGCTCCAC 1500
Qy 1501 CCAATTCAGACTTGCACATATATGTCGATGGCCAGAGGGGTAATAATGATAT 1560
Db 1501 CCAATTCAGACTTGCACATATATGTCGATGGCCAGAGGGGTAATAATGATAT 1560
Qy 1561 GTGCGGAAACATTAAGCTGGCCAGATGAGATATCAACGAAATAGCTGTGACC 1620
Db 1561 GTGCGGAAACATTAAGCTGGCCAGATGAGATATCAACGAAATAGCTGTGACC 1620
Qy 1621 GTACACATTAATGAGATGGTGGGGGAAATTCATCTGTAACGAGAGGGGAGTTGGTT 1680
Db 1621 GTACACATTAATGAGATGGTGGGGGAAATTCATCTGTAACGAGAGGGGAGTTGGTT 1680
Qy 1681 TGGGTAGAGCAATTAATTAAGAAACAAGGCGAAATTAATCTTCTTCAATGACAGCTTT 1740
Db 1681 TGGGTAGAGCAATTAATTAAGAAACAAGGCGAAATTAATCTTCTTCAATGACAGCTTT 1740
Qy 1741 CCGATCACTCATACACCCCAATTAATTTGAGACTT 1776
Db 1741 CCGATCACTCATACACCCCAATTAATTTGAGACTT 1776

RESULT 3
AAC66234
ID AAC66234 standard; DNA; 1786 BP.
AC AAC66234;
XX
DT 19-FEB-2001 (first entry)
XX
DE Mutant alpha-amylase nucleotide sequence.
XX
KW Alpha-amylase; detergent; Bacillus; ds.
XX
OS Bacillus sp.
XX
PN JP2000245466-A.
PD 12-SEP-2000.
XX
PF 25-FEB-1999; 99JP-00048213.
XX
PR 25-FEB-1999; 99JP-00048213.
XX
PA (KAOS) KAO CORP.
XX
DR MPI; 2000-615143/59.
XX
DR F-PSDB; AAB35714.
XX
PT A novel mutant alpha-amylase for use in a detergent composition.
XX
PS Example 1; Page 6-9; 12pp; Japanese.
XX
CC The present invention relates to a mutant alpha-amylase. Included in the
CC invention are a gene encoding the mutant alpha-amylase, a vector
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CC containing the gene, and a transformed cell recombinant by the vector. The
CC enzyme is used in a detergent composition. The present sequence
CC represents the mutant alpha-amylase gene
XX
SQ Sequence 1786 BP; 578 A; 307 C; 420 G; 481 T; 0 U; 0 Other;
Query Match 100.0%; Score 1776; DB 3; Length 1786;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1776; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATATTAATTTGAATGAACACCTATGAATATATGATGATGGGCGACGAGAAAAC 60
Db 11 ATATTAATTTGAATGAACACCTATGAATATATGATGATGGGCGACGAGAAAAC 70
Qy 61 TTGGAGATTAGAGAGATATTAAGAAATTTTGTGACTTGTGTGAACGCTTGCA 120
Db 71 TTGGAGATTAGAGAGATATTAAGAAATTTTGTGACTTGTGTGAACGCTTGCA 130
Qy 121 AAATTGAAGAGAGGAGCTTTTATGAACCTTCAATACCGTATTAATGCTATTA 180
Db 131 AAATTGAAGAGAGGAGCTTTTATGAACCTTCAATACCGTATTAATGCTATTA 190
Qy 181 ACACTATTGTAGCTGTAGCTGTTTGTTCATATATGACGAGAACGACAGCCCAT 240
Db 191 ACACTATTGTAGCTGTAGCTGTTTGTTCATATATGACGAGAACGACAGCCCAT 250
Qy 241 CATTAATGGAGAGATAGGACCATGATGAGTATTTGAATGSCATTTGGCAATGACGG 300
Db 251 CATTAATGGAGAGATAGGACCATGATGAGTATTTGAATGSCATTTGGCAATGACGG 310
Qy 301 AACCACTGGAAACAGTTACGAGATGACGAGCTAACTTAAGATTAAGAGATTAACGCT 360
Db 311 AACCACTGGAAACAGTTACGAGATGACGAGCTAACTTAAGATTAAGAGATTAACGCT 370
Qy 361 GTTTGATTTCTTCCTGCAATGAGAGGAGCTTGGCAAAATGATGTTGGTATGCTAT 420
Db 371 GTTTGATTTCTTCCTGCAATGAGAGGAGCTTGGCAAAATGATGTTGGTATGCTAT 430
Qy 421 GATTTGATGATCTTGTGATGTTTAACCAAAAGGAGCCGTCCTTCAAAATATGAGCA 480
Db 431 GATTTGATGATCTTGTGATGTTTAACCAAAAGGAGCCGTCCTTCAAAATATGAGCA 490
Qy 481 AGGAGTCAGTTGCAAGTGGCGCTGACATCTTTGAATTAACGAGATTAACGATTA 540
Db 491 AGGAGTCAGTTGCAAGTGGCGCTGACATCTTTGAATTAACGAGATTAACGATTA 550
Qy 541 GATGTCGTGATGAATCATTAAGTGGAGACAGCGGACAGATGTTAATGGGAGAA 600
Db 551 GATGTCGTGATGAATCATTAAGTGGAGACAGCGGACAGATGTTAATGGGAGAA 610
Qy 601 GTGAACCGAAGCAACGAAACCAAGAAATATAGGATGAATACACATTTGAGATGAGC 660
Db 611 GTGAACCGAAGCAACGAAACCAAGAAATATAGGATGAATACACATTTGAGATGAGC 670
Qy 661 AAATTTGATTTCTTGGAAAGAGAAATTAATCCATTCACATTTAATGCGCTGTATCAT 720
Db 671 AAATTTGATTTCTTGGAAAGAGAAATTAATCCATTCACATTTAATGCGCTGTATCAT 730
Qy 721 TTTGATGGAGACATTTGGATCATGTCACCTGACCTTGAACAAATATATTAATTCGA 780
Db 731 TTTGATGGAGACATTTGGATCATGTCACCTGACCTTGAACAAATATATTAATTCGA 790
Qy 781 GGTAACCGAAGAGAGGAGCTGGAGAGTATATAGAAACGCAACTATGATTAACCTT 840
Db 791 GGTAACCGAAGAGAGGAGCTGGAGAGTATATAGAAACGCAACTATGATTAACCTT 850
Qy 841 ATGATGACAGATTTGATGATCATCCAGAGATTAATGAATGAAATTTGGAG 900
Db 851 ATGATGACAGATTTGATGATCATCCAGAGATTAATGAATGAAATTTGGAG 910
Qy 901 GTTTGGTATTAACAATTAACATTAATCTAGATGATTTGAATGATGCTGTGAACATATT 960
Db 911 GTTTGGTATTAACAATTAACATTAATCTAGATGATTTGAATGATGCTGTGAACATATT 970
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QY 961 AAATACGCTATACGAGATTGGCTAACACATGCGCTAACACCAAGGTAACCAATG 1020
 DB 971 AAATACGCTATACGAGATTGGCTAACACATGCGCTAACACCAAGGTAACCAATG 1030
 QY 1021 TTTCAGTTCGAGATTTTGGAAAAATGACCTTCGCAATCGAAAACTATTATTAATAA 1080
 DB 1031 TTTCAGTTCGAGATTTTGGAAAAATGACCTTCGCAATCGAAAACTATTATTAATAA 1090
 QY 1081 ACAAGTTGGAATCACTCCGTTGATGTTCTCTCTCAATTAATTTGTACATGATCT 1140
 DB 1091 ACAAGTTGGAATCACTCCGTTGATGTTCTCTCTCAATTAATTTGTACATGATCT 1150
 QY 1141 AATAGTGGTGGCTTTTGTATATGAAATTTTAAATGGTTCGTCGTAACAAAACAC 1200
 DB 1151 AATAGTGGTGGCTTTTGTATATGAAATTTTAAATGGTTCGTCGTAACAAAACAC 1210
 QY 1201 CCTATACATGACATGACATTTTGTATATGAAATGCTCTCAGCCAGAGAAACATTTGAA 1260
 DB 1211 CCTATACATGACATGACATTTTGTATATGAAATGCTCTCAGCCAGAGAAACATTTGAA 1270
 QY 1261 TCCCTTTGTTCAATGCTGTTGAAACCACTGCGATATGCAATGATTCTGCAAGGAGCAA 1320
 DB 1271 TCCCTTTGTTCAATGCTGTTGAAACCACTGCGATATGCAATGATTCTGCAAGGAGCAA 1330
 QY 1321 GGTACACCTTCCGTAATTTTAAAGGTATACAGGTATACCAACTCATGTTCTCTCG 1380
 DB 1331 GGTACACCTTCCGTAATTTTAAAGGTATACAGGTATACCAACTCATGTTCTCTCG 1390
 QY 1381 ATGAATATCTAAATTTGATCTCACTCTGCAAGGACGTCMAAGTATGCTACGAAACCAA 1440
 DB 1391 ATGAATATCTAAATTTGATCTCACTCTGCAAGGACGTCMAAGTATGCTACGAAACCAA 1450
 QY 1441 CATGATTTTGTATCATCATGATATTTTGGCTGAGACGAGAAAGGAGACGCTCCAC 1500
 DB 1451 CATGATTTTGTATCATCATGATATTTTGGCTGAGACGAGAAAGGAGACGCTCCAC 1510
 QY 1501 CCAATTTCAAGACTTGGCAACTATATGCGCATGCGGCGCAAGGGGTAATTAATGATGAT 1560
 DB 1511 CCAATTTCAAGACTTGGCAACTATATGCGCATGCGGCGCAAGGGGTAATTAATGATGAT 1570
 QY 1561 GTCGGGAAACATTAAGCTGCGCAAGTATGAGAGATATCAACGGAATAGGTCTGATCC 1620
 DB 1571 GTCGGGAAACATTAAGCTGCGCAAGTATGAGAGATATCAACGGAATAGGTCTGATCC 1630
 QY 1621 GTCACCATTAATGACATGTTGGGGGAATTTCACTGTAAACGAGGGGCAAGTTCCGTT 1680
 DB 1631 GTCACCATTAATGACATGTTGGGGGAATTTCACTGTAAACGAGGGGCAAGTTCCGTT 1690
 QY 1681 TGGGTGAAGCAATTAATTAAGAACAGAGGGAATTAATCTTCTCAATGACAGATCTT 1740
 DB 1691 TGGGTGAAGCAATTAATTAAGAACAGAGGGAATTAATCTTCTCAATGACAGATCTT 1750
 QY 1741 CCGATCACTCATACACCAATATTAATTTGAAGCTT 1776
 DB 1751 CCGATCACTCATACACCAATATTAATTTGAAGCTT 1786
 RESULT 4
 AAK9881
 ID AAK9881 standard; DNA; 1786 BP.
 XX
 AC AAK9881;
 XX
 DT 19-JUL-2002 (first entry)
 XX
 DE DNA of Bacillus sp alpha-amylase KSM-API378 (FERM BP-3048) protein.
 XX
 KW Alpha-amylase; detergent; laundry; bleaching; dishwashing; enzyme;
 XX fibre desizing; starch liquefaction; KSM-API378; FERM BP-3048; gene; ds.
 OS Bacillus sp.
 XX

FH Key Location/Qualifiers
 FT CDS 155..1705
 FT /tag= a
 FT /product= "Bacillus sp. alpha-amylase KSM-API378 (FERM BP
 FT -3048) protein"
 FT sig_peptide 155..247
 FT /tag= b
 FT /note= "Not shown in the specification"
 FT mat_peptide 248..1702
 FT /tag= c
 XX
 PN EPI199356-A2.
 XX
 PD 24-APR-2002.
 XX
 PF 10-OCT-2001; 2001EP-00123378.
 XX
 PR 11-OCT-2000; 2000JP-00310605.
 XX
 PA (KAO) KAO CORP.
 XX
 PI Araki H, Hagihari H, Hayashi Y, Endo K, Igarashi K, Ozaki K;
 DR WPI; 2002-354203/39.
 DR P-PSDB; AAO21000.
 XX
 PT New mutant alpha-amylase, useful in detergent compositions, comprises
 PT increased productivity when prepared recombinantly and better resistance
 PT to heat.
 PS
 XX
 PS Disclosure; Page 21-25; 45pp; English.
 CC
 CC The invention relates to a mutant alpha-amylase derived from a fully
 CC defined sequence of 485 amino acids or a 480 aa sequence as given in the
 CC specification by substitution or deletion of one or more specified amino
 CC acids. The mutant amylase proteins of the invention can be produced at a
 CC high yield from a recombinant organism, making it possible to drastically
 CC reduce the cost of their production. The mutant amylase proteins are
 CC useful in detergent compositions (e.g. laundry, bleaching and dishwashing
 CC compositions), also for liquefaction of starch and desizing fibres.
 CC optionally used in conjunction with other enzymes. This polynucleotide
 CC sequence represents DNA encoding the 485 amino acid Bacillus sp. alpha-
 CC amylase KSM-API378 (FERM BP-3048) protein of the invention
 XX
 SO Sequence 1786 BP; 578 A; 307 C; 420 G; 481 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1776; DB 6; Length 1786;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1776; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATATTAATTTGGAATGAACACCTATGTAATATGTAAGGTAACGTAATTAATTAAGGTAATTA 180
 DB 11 ATATTAATTTGGAATGAACACCTATGTAATATGTAAGGTAACGTAATTAATTAAGGTAATTA 190
 QY 61 TTGGAGATTGGAAGTATTAAGGATTTTGTGACTTGTGTAAGGATTTGTAAGGATTTGTAAGGATTT 120
 DB 71 TTGGAGATTGGAAGTATTAAGGATTTTGTGACTTGTGTAAGGATTTGTAAGGATTTGTAAGGATTT 130
 QY 121 AAATTAAGAGAGAGGCTTTTATGAACTTATACCACTGTAATTAATTAAGGTAATTA 180
 DB 131 AAATTAAGAGAGAGGCTTTTATGAACTTATACCACTGTAATTAATTAAGGTAATTA 190
 QY 181 ACATTAATTTGTAAGTATTAAGGATTTTGTGACTTGTGTAAGGATTTGTAAGGATTTGTAAGGATTT 240
 DB 191 ACATTAATTTGTAAGTATTAAGGATTTTGTGACTTGTGTAAGGATTTGTAAGGATTTGTAAGGATTT 250
 QY 241 CATATGGAAGCAATGGAAGCAATGGAAGCAATGGAAGCAATGGAAGCAATGGAAGCAATGGAAGCAAT 300
 DB 251 CATATGGAAGCAATGGAAGCAATGGAAGCAATGGAAGCAATGGAAGCAATGGAAGCAATGGAAGCAAT 310
 QY 301 AACCACTGGAACAGGTATGAGATGACGACGACTTAATTAAGGTAATTAAGGATTTACGCT 360
 DB 311 AACCACTGGAACAGGTATGAGATGACGACGACTTAATTAAGGTAATTAAGGATTTACGCT 370

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QY 361 GTTGGATTCTCCGTCATGGAAGGGGACTTGGCAAAATGATGTGGGTATGCGCTCAT 420
Db 371 GTTGGATTCTCTCTGATGGAAGGGGACTTGGCAAAATGATGTGGGTATGCGCTCAT 430
QY 421 GATTGTAGCATCTTGGTGTAGTTAACCAAAAGGGAACCGTCCGTCAAAATATGCGACA 480
Db 431 GATTGTAGCATCTTGGTGTAGTTAACCAAAAGGGAACCGTCCGTCAAAATATGCGACA 490
QY 481 AGAGTCAGTTGGAAGGTGCGGTGACATCTTTGAAAATTAACGGGATCAAGTTATGGG 540
Db 491 AGAGTCAGTTGGAAGGTGCGGTGACATCTTTGAAAATTAACGGGATCAAGTTATGGG 550
QY 541 GATGTGTGATGATCATAAAGGTGAGCAGGAGCAGAGATGGTAAATGCGGTGAA 600
Db 551 GATGTGTGATGATCATAAAGGTGAGCAGGAGCAGAGATGGTAAATGCGGTGAA 610
QY 601 GTGAAACCGAAGCAACCGAAACCAAGAAATATCAGTGAATACCAATTGAAAGCATGAGC 660
Db 611 GTGAAACCGAAGCAACCGAAACCAAGAAATATCAGTGAATACCAATTGAAAGCATGAGC 670
QY 661 AATTTGATTTCCCTGGAAAGGAATATCCCATTTCAACTTTAAATGGGCTGTGATCAT 720
Db 671 AATTTGATTTCCCTGGAAAGGAATATCCCATTTCAACTTTAAATGGGCTGTGATCAT 730
QY 721 TTGATGGGACAGATTGGGATCAGTCACGTCAGCTTCAGAACCAAAATATTAATTCAGA 780
Db 731 TTGATGGGACAGATTGGGATCAGTCACGTCAGCTTCAGAACCAAAATATTAATTCAGA 790
QY 781 GGTACCGGAAAGGCATGGGACTGGGAAGTATGATATAGAAACGGCAACTATGATTAACCTT 840
Db 791 GGTACCGGAAAGGCATGGGACTGGGAAGTATGATATAGAAACGGCAACTATGATTAACCTT 850
QY 841 AAGTATGAGACATTTGATATGATCATCCGAAGTATCAATGAACTTGAATTTGGGA 900
Db 851 AAGTATGAGACATTTGATATGATCATCCGAAGTATCAATGAACTTGAATTTGGGA 910
QY 901 GTTGGTATACAAATACACTTATCTAGATGATTAAGATCGATCTGTGAACATATTT 960
Db 911 GTTGGTATACAAATACACTTATCTAGATGATTAAGATCGATCTGTGTGAACATATTT 970
QY 961 AATATACGCTATACGAGAATTTGGCTPAACATGTGCTGPAACCAACAGTAAACCAATG 1020
Db 971 AATATACGCTATACGAGAATTTGGCTPAACATGTGCTGPAACCAACAGTAAACCAATG 1030
QY 1021 TTGCGATGGCAATTTTGGAAATATGACCTGTGCGAATGGAAACATATTAATTA 1080
Db 1031 TTGCGATGGCAATTTTGGAAATATGACCTGTGCGAATGGAAACATATTAATTA 1090
QY 1081 ACAAGTTGGATCACTCCGTTGCGATGTTCCCTCATTTATTAATTTGTAACATGATCT 1140
Db 1091 ACAAGTTGGATCACTCCGTTGCGATGTTCCCTCATTTATTAATTTGTAACATGATCT 1150
QY 1141 AATAGTGTGGCTATTTTGTATGAGAATATTTAAATGTGTCTGTCTGCAAAAACAC 1200
Db 1151 AATAGTGTGGCTATTTTGTATGAGAATATTTAAATGTGTCTGTCTGCAAAAACAC 1210
QY 1201 CCTATACATGACATCAATTTGTTGATTAACATGACCTTCAGCAGAGAGACATTTGAA 1260
Db 1211 CCTATACATGACATCAATTTGTTGATTAACATGACCTTCAGCAGAGAGACATTTGAA 1270
QY 1261 TCCTTTGTCAATCGTGTCAAAACCACTGGCATATGATGATTTGCAAGGAGCAA 1320
Db 1271 TCCTTTGTCAATCGTGTCAAAACCACTGGCATATGATGATTTGCAAGGAGCAA 1330
QY 1321 GGTACCCCTTCGATATTTACGGTATTAACGATACCAACATGATGTTCTCTTG 1380
Db 1331 GGTACCCCTTCGATATTTACGGTATTAACGATACCAACATGATGTTCTCTTG 1390
QY 1381 ATGAATCTTAAATTTATCATCTTGTGCGAGGACGTCAAACGATATCGGAACCCAA 1440
Db 1391 ATGAATCTTAAATTTATCATCTTGTGCGAGGACGTCAAACGATATCGGAACCCAA 1450

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QY 1441 CATGATTATTTGATCATGATATTAATCGGCTGAGCAGAGAAAGGGACAGCTCCAC 1500
Db 1451 CATGATTATTTGATCATGATATTAATCGGCTGAGCAGAGAAAGGGACAGCTCCAC 1510
QY 1501 CCAATTCAGACTTGCAACTATTAATGTCGATGGGCCAGGGGGTAAATATGATGTAT 1560
Db 1511 CCAATTCAGACTTGCAACTATTAATGTCGATGGGCCAGGGGGTAAATATGATGTAT 1570
QY 1561 GTGGGGAACATTAAGCTGGCCAGATATGAGAGATATCACCGGAAATAGTCTGGTAC 1620
Db 1571 GTGGGGAACATTAAGCTGGCCAGATATGAGAGATATCACCGGAAATAGTCTGGTAC 1630
QY 1621 GTACACATTAATGAGATGTTGGGGGAATTTCACTGTAAACGAGGGGCACTTCCGTT 1680
Db 1631 GTACACATTAATGAGATGTTGGGGGAATTTCACTGTAAACGAGGGGCACTTCCGTT 1690
QY 1681 TGGGTGAGCAATTAATTAAGGAACAAGGGGCAAAATTAATTTCTTCTACATGACGCTTT 1740
Db 1691 TGGGTGAGCAATTAATTAAGGAACAAGGGGCAAAATTAATTTCTTCTACATGACGCTTT 1750
QY 1741 CCGATCCTCATACACCCCAATTAATTTGGAAGCTT 1776
Db 1751 CCGATCCTCATACACCCCAATTAATTTGGAAGCTT 1786

RESULT 5
AAD49392/c
ID AAD49392 standard; DNA; 6661 BP.
AC AAD49392;
XX 07-MAR-2003 (first entry)
XX
DE pMO2995 plasmid DNA.
XX
KW Pectate lyase; EC 4.2.2.2; detergent; surfactant; cleaning; dishwashing;
KW fabric stain removal; fabric whiteness maintenance; fabric softening;
KW fabric colour appearance; fabric dye transfer inhibition; de-pilling;
KW dental application; oral application; colour clarification; enzyme;
KW clay stain removal; ds.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT 1..1962 misc_feature
FT /tag= a
FT /note= "Encodes PUB110 plasmid"
FT 1963..2305 terminator
FT /tag= b
FT /note= "Encodes transcriptional terminator from amyL gene
FT of B. licheniformis ATCC14580 and a few introduced
FT restriction sites"
FT 2306..3766 misc_feature
FT /tag= c
FT /note= "Encodes mature part of alpha-amyase"
FT complement (3767..4075)
FT /tag= d
FT /note= "Encodes the promoter and signalpeptide of alpha-
FT amyase"
FT 4076..6661 misc_feature
FT /tag= e
FT /note= "Encodes PUB110 plasmid"
PN MO20029741-A2.
XX
PD 21-NOV-2002.
XX
XX 14-MAY-2002; 2002WO-DK000315.
XX
PF 14-MAY-2001; 2001DK-00000755.
PR 14-MAY-2001; 2001US-0290738P.
XX
XX (NOVO ) NOVOZYMES AS.
PA

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XX DE Bacillus sp. alkaline alpha-amylase DNA.
 XX KW Alpha-amylase; enzyme; EC-3.2.1.1; detergent; surfactant; textile; beer;
 XX KW starch; ss.
 XX OS Bacillus.
 XX PN MO9526397-A1.
 XX PF 29-MAR-1995; 95WO-DK000142.
 XX PR 29-MAR-1994; 94DK-00000353.
 XX PR 03-NOV-1994; 94DK-00001271.
 XX PR 03-FEB-1995; 95DK-00000123.
 XX PA (NOVO) NOVO-NORDISK AS.
 XX PI Outtrup H, Bisgard-Frantzen H, Ostergaard PR, Rasmussen MD;
 XX PI Van Der Zee P;
 XX DR MPI; 1995-351318/45.
 XX DR P-PSDB; AAR81835.
 XX PT New alkaline Bacillus alpha-amylase - used in e.g. detergent compen-
 XX PT starch liquefaction, textile desizing, starch modification or beer
 XX PT making.
 XX PS Disclosure; Page 48-49; 65pp; English.
 XX CC This DNA sequence may be expressed recombinantly for the production of an
 XX CC alpha-amylase protein. The produced protein is characterized by having a
 XX CC specific activity at least 25% higher than the specific activity of
 XX CC Termamyl at 25-55 deg C and a pH of 8-10. The enzyme can be used in
 XX CC detergent composition for starch liquefaction, the production of
 XX CC lignocellulosic materials, e.g. pulp, paper and cardboard from waste
 XX CC containing starch, for deinking recycled starch-coated, or starch-
 XX CC containing printed paper, to modify starch for papermaking, for textile
 XX CC desizing, and beer-making processes
 XX CC
 XX SQ Sequence 1455 BP; 461 A; 248 C; 361 G; 385 T; 0 U; 0 Other;
 Query Match 65.7%; Score 1167; DB 2; Length 1455;
 Best Local Similarity 87.6%; Pred. No. 2.5e-307;
 Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0;
 QY 238 CATCATATGGAAGATGGAGATGGACCATGATGACATATTTGATGGATTGGCCAAATGAC 297
 DB 1 CATCATATGGAAGATGGAGATGGACCATGATGACATATTTGATGGATTGGCCAAATGAC 60
 QY 298 GGGAGCACTGGAGCAAGGTTACGAGATGACGACGCTAATTAAAGATTAAGGATACC 357
 DB 61 GGGAGCACTGGAGCAAGGTTACGAGATGACGACGCTAATTAAAGATTAAGGATTAAGG 120
 QY 358 GCGTTTGGATTCCTCGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 417
 DB 121 GCGTTTGGATTCCTCGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
 QY 418 TATGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 477
 DB 181 TATGATTTATATATCTTGGAGAGTTTAAACAGAGAGGAGGAGGAGGAGGAGGAGGAGG 240
 QY 478 ACAAGAGTCATGTTGCAAGGTGCGGTGACATCTTTGAAAATTAACGGAGTTCAAGTTAT 537
 DB 241 ACAACGAAACAGCTACAGGCTGGGTGACCTCTTTAAAAATTAACGGCATTCAGGTATAT 300
 QY 538 GGGAGAGTCGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 597
 DB 301 GGTGATGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
 QY 598 GAAGTGAACCGAAGCAACCGAAGCAAGAAATATCAGTGAATTAACCATTTGAAGCATGG 657

DB 361 GAAGTGAACCGAAGCAACCGAAGCAAGAACTCAGAGAGATATGCAATAGAGGTGG 420
 QY 658 ACGAAATTTGATTTCCCTGGAGAGAGAAATACCATTTCACTTTAATGGCGTGTAT 717
 DB 421 ACGAAATTTGATTTCCCTGGAGAGAGAAATACCATTTCACTTTAATGGCGTGTAT 480
 QY 718 CATTTTATGAGGACGATTTGGGATCAGTCAAGCTTCAGAACCAAAATATATTAATTC 777
 DB 481 CATTTTATGAGGACGATTTGGGATCAGTCAAGCTTCAGAACCAAAATATATTAATTC 540
 QY 778 AGAGTACCGGAAGGATGGAGCTGGAGATGATATAGAGAGCGCAACTATGATTAC 837
 DB 541 AGGGGAAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
 QY 838 CTTATGATGACGACATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 897
 DB 601 CTTATGATGACGACATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
 QY 898 GGAGTTGGTATCAAAATCACTTAATCTAGATGATGATGATGATGATGATGATGATGAT 957
 DB 661 GGAGTTGGTATCAAAATCACTTAATCTAGATGATGATGATGATGATGATGATGATGAT 720
 QY 958 ATTAATATACAGCTATACAGAGATTTGCTTACATATGTCGTACACCAAGATAACCA 1017
 DB 721 ATTAATATATAGCTTATACAGAGATTTGCTTACATATGTCGTACACCAAGATAACCA 780
 QY 1018 ATGTTTGCAGTTGCAGATTTTGGAAAAATGACCTTTCGTCGATGAGAAATCTTTAAT 1077
 DB 781 ATGTTTGCAGTTGCAGATTTTGGAAAAATGACCTTTCGTCGATGAGAAATCTTTAAT 840
 QY 1078 AAAACAAGTTGGAATCACTCCGTTGTCATGATGATGATGATGATGATGATGATGATGAT 1137
 DB 841 AAAACAAGTTGGAATCACTCCGTTGTCATGATGATGATGATGATGATGATGATGATGAT 900
 QY 1138 TCTAATAGTGTGGCTATTTGATATGAGAAATATTTAATGTTGTCGTACAAAAA 1197
 DB 901 TCTAATAGTGTGGCTATTTGATATGAGAAATATTTAATGTTGTCGTACAAAAA 960
 QY 1198 CACCTATATCAGTCACTATTTGTTGATATCAATGATCTCAGCCAGAGAAAGATTG 1257
 DB 961 CATCAACACATGCGGTTATCTTTGTTGATATCAATGATCTCAGCCAGAGAAAGATTG 1020
 QY 1258 GAATCCTTTGTCATATCGTGTGTTCAACACCTGAGATGATGATGATGATGATGATGATGAT 1317
 DB 1021 GAATCCTTTGTCATATCGTGTGTTCAACACCTGAGATGATGATGATGATGATGATGATGAT 1080
 QY 1318 CAAGTTTACCTTCGATATTTTACGATGATTAATCAAGGATTAACCACTGATGATGAT 1377
 DB 1081 CAAGTTTATCTTCGATATTTTATGAGGATTAATCAAGGATTAACCACTGATGATGAT 1140
 QY 1378 TCGATGAAATCTAAATGATCACTTCGACAGGACCGTCAACGATATGCTTAACGAAAC 1437
 DB 1141 GGTATGAAATCTAAATGATCACTTCGACAGGACCGTCAACGATATGCTTAACGAAAC 1200
 QY 1438 CAACATGATTTTATGATCATGATATTTATCGCTGAGACAGAGAGGAGGAGGAGGAGG 1497
 DB 1201 CAGCATGATTTATGATCATGATATTTATCGCTGAGACAGAGAGGAGGAGGAGGAGGAGG 1260
 QY 1498 CACCAATTCAGACTTGCAATTAATGTCGATGAGGACGAGGAGGATTAATATGATG 1557
 DB 1261 CATCAAAATTCAGACTTGCAATTAATGTCGATGAGGACGAGGAGGATTAATATGATG 1320
 QY 1558 TATGTCGGGAAACATTAAGCTGGGCAAGATGAGAGATATCAACGGAAATGAGTGTG 1617
 DB 1321 TATGTCGGGAAACATTAAGCTGGGCAAGATGAGAGATATTAACGGAAATGAGAGGAGG 1380
 QY 1618 ACCGTCAACATTAATGAGATGTTGGGGAATTTCACTGTAACGAGAGGAGGAGGAGGAGG 1677
 DB 1381 ACCGTCAACATTAATGAGATGTTGGGGAATTTCTCTGTTAATGAGAGGAGGAGGAGGAGG 1440
 QY 1678 GTTGGGTGAAGCAA 1692

Db 1441 GTTGGTGGAAGCAA 1455

RESULT 7

AA59636
ID AAX59636 standard; DNA; 1455 BP.

AC AAX59636;

DT 22-JUL-1999 (first entry)

DE DNA encoding a termamyl-like alpha-amylase protein.

KM Termamyl-like; alpha-amylase; variant; washing; dishwashing; production;

KM sweetener; ethanol; starch; textile desizing; starch liquefaction;

KM saccharification process; ss.

OS Bacillus sp.

PN MO9923211-A1.

PD 14-MAY-1999.

PF 30-OCT-1998; 98WO-DK000471.

PR 30-OCT-1997; 97DK-00001240.

PR 14-JUL-1998; 98DK-00000936.

PA (NOVO) NOVO-NORDISK AS.

PI Borchert TV, Svendsen A, Andersen C, Nielsen BR, Nissen TL;

PI Kjaerulff S;

DR WPI; 1999-326987/27.

PS New Termamyl-like alpha-amylase variants.

XX Disclosure; Page 98; 115pp; English.

XX The specification describes termamyl-like alpha-amylase variants that

CC have altered amino acid sequences to improve properties. The variants are

CC produced by creating one or more of the following mutations in amino acid

CC sequence of the parent termamyl-like alpha-amylase: T141, K142, F143,

CC D144, F145, P146, G147, R148, G149, Q174, R181, G182, D183, G184, K185,

CC A186, W188, S193, N195, H107, K108, G109, D166, W167, D168, Q169, S170,

CC R171, Q172, F173, F267, W268, K269, N270, D271, L272, G273, A274, L275,

CC K311, E346, K385, G456, N457, K458, P459, G460, T461, V462, T463. The

CC variants can be used for washing and/or dishwashing. They can also be

CC used in the production of sweeteners and ethanol from starch, and/or for

CC textile desizing, and in starch liquefaction and/or saccharification as

CC processes. The present sequence encodes an amylase that can function as

CC the parent sequence in the production of the variants of the invention

XX Sequence 1455 BP; 461 A; 248 C; 361 G; 385 T; 0 U; 0 Other;

SO Query Match 65.7%; Score 1167; DB 2; Length 1455;

Best Local Similarity 87.6%; Pred. No. 2.5e-307;

Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

Db 181 TATGATTTATATGATCTTGGAGAGTTTAAACGAGGGAACGGTTCGTACAAATATGGA 240

Qy 478 ACAGAGTACAGTTCGCAAGGTCGGTGAACATCTTGAATAATACGGGATTCAGTTTAT 537

Db 241 ACAGCAACAGCTACAGGCTGGGTGACCTTTTAAAAATACGGCATTCAGATTTAT 300

Qy 538 GGGATGTCGTATGATATCAATTAAGTGGAGCAGACGGACAGAGATGTGTAATGCGGTG 597

Db 301 GGTATGTCGTATGATATCAATTAAGTGGAGCAGATGTGTAATGCGGTG 360

Qy 598 GAAGTGAACCGAAGCAACCGAAGCAATATACAGTGAATACCATTTAGAACATGG 657

Db 361 GAAGTGAATCGAGACCAACCGAAGCAACCTCAGAGAGTATGCAATGAAACCGTGG 420

Qy 658 ACGAAATTTGATTTCCCTGGAGAGGAAATACCATTCGAACTTAAATGCGGTGAT 717

Db 421 ACAAAGTTTGAATTTCTGGAGAGGAAATACCATTCGAACTTAAATGCGGTGAT 480

Qy 718 CATTTTATGAGGACAGATGGGATCAGTCAAGTCAAGTTCAGAACAAATATATATTC 777

Db 481 CATTTTATGAGGACAGATGGGATCAGTCAAGTCAAGTTCAGAACAAATATATATTC 540

Qy 778 AGAGTACCGGAAAGGACATGGGACCTGGGAAGTATAGAAAGGCAACTATGATTAC 837

Db 541 AGGGAACAGGCAAGGCTGGGACCTGGGAAGTATAGAAAGGCAACTATGATTAC 600

Qy 838 CTTATATGATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 897

Db 601 CTTATATGATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660

Qy 898 GGAGTTTGTATCAATATACCTTAATCTAGATGATGATGATGATGATGATGATGATG 957

Db 661 GGAGTTTGTATCAATATACCTTAATCTAGATGATGATGATGATGATGATGATGATG 720

Qy 958 ATTTAATACAGCTTATACGAGATGAGTGGCTAACACATGTCGTAAACACAGTAAACA 1017

Db 721 ATTTAATACAGCTTATACGAGATGAGTGGCTTAACACATGTCGTAAACACAGTAAACA 780

Qy 1018 ATGTTTGCAGTGCAGAAATTTTGGAAAAATGACCTTGTGCAATGAAACTATTTAAT 1077

Db 781 ATGTTTGCAGTGCAGAAATTTTGGAAAAATGACCTTGTGCAATGAAACTATTTAAT 840

Qy 1078 AAAACAAGTTGGATTCAGCTCGTTCGATGATGATGATGATGATGATGATGATGATG 1137

Db 841 AAAACAAGTTGGATTCAGCTCGTTCGATGATGATGATGATGATGATGATGATGATG 900

Qy 1138 TCTATATGAGTGGCTATTTTGTATGATGAGAAATTTTAAATGTTCTGTGTCGTA 1197

Db 901 TCTATATGAGTGGCTATTTTGTATGATGAGAAATTTTAAATGTTCTGTGTCGTA 960

Qy 1198 CACCTTATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1257

Db 961 CACCTTATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020

Qy 1258 GAATCCTTTGTTCAATGCTGTTCAACCACTGGCATATGATGATGATGATGATGATG 1317

Db 1021 GAATCCTTTGTTCAACCAATGTTTAAACCACTGGCATATGATGATGATGATGATGATG 1080

Qy 1318 CAAGTTTACCTTCGATATTTTACGATGATGATGATGATGATGATGATGATGATGATG 1377

Db 1081 CAAGTTTATCCTTCGATATTTTATGAGGATTTACACGATATCCAACCAATGTTTCCG 1140

Qy 1378 TCGATGAATCTTAAATGATTCACCTTCGAGGACGTCACACGATATGCTTACGAAAC 1437

Db 1141 GCTATGAATCTTAAATGATTCACCTTCGAGGACGTCACACCTTTTGTCTATGATACG 1200

Qy 1438 CAATGATATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1497

Db 1201 CAGATATATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1260

Qy 1498 CACCAAAATTCAGACTTGCACATTTATGTCGATGGGACAGGGGCTAAATTAATGATG 1557

Db 1261 CATCAAAATTCAGACTTGCACATTTATGTCGATGGGCTAAATTAATGATGATG 1320

QY 1558 TATGCGGAGAAACATTAAGCTGGCCAAGTATGAGAGATATCAACCGAAATAGCTGCGT 1617
DB 1321 TATGTGGGAAAAAATAAGCGGAGACAGATTGTGAGAGATTTACCGAAATAGAGACGCG 1380
QY 1618 ACCGTACCATTAATGAGATGGTGGGGAATTTCACTGTAAACGAGGGGAGATTGCG 1677
DB 1381 ACCGTACCATTAATGAGAGATGGGGAATTTCTGTATATGAGAGGCGTTCGTTGCG 1440
QY 1678 GTTGGGTGAAGCA 1692
DB 1441 GTTGGGTGAAGCA 1455

RESULT 8
AAK59632
ID AAK59632 standard; DNA; 1455 BP.
XX AAK59632;
XX
XX
DT 22-JUL-1999 (first entry)
XX
DE DNA encoding a termamyl-like alpha-amylase protein.
XX
XX Termamyl-like; alpha-amylase; variant; washing; dishwashing; production;
KM sweetener; ethanol; starch; textile desizing; starch liquefaction;
XX saccharification process; ss.
XX
OS Bacillus sp.
XX
XX W09923211-A1.
XX
PD 14-MAY-1999.
XX
PF 30-OCT-1998; 98MO-DK000471.
XX
XX 30-OCT-1997; 97DK-00001240.
PR 14-JUL-1998; 98DK-00000936.
XX
XX (NOVO) NOVO-NORDISK AS.
XX
XX Borchert TV, Svendsen A, Andersen C, Nielsen BR, Nissen TV;
PI Kjaerulff S;
XX
DR WPI; 1999-326987/27.
XX
XX
PT New Termamyl-like alpha-amylase variants.
XX
PS Disclosure; Page 91-92; 115pp; English.
XX
XX The specification describes termamyl-like alpha-amylase variants that
CC have altered amino acid sequences to improve properties. The variants are
CC produced by creating one or more of the following mutations in amino acid
CC sequence of the parent termamyl-like alpha-amylase: T141, K142, F143,
CC D144, F145, P146, G147, R148, G149, Q174, R181, G182, D183, G184, K185,
CC A186, W189, S193, N195, H107, K108, G109, D166, W167, D168, Q169, S170,
CC R171, Q172, F173, P267, W268, K269, N270, D271, L272, G273, A274, L275,
CC K311, E346, K385, G456, N457, K458, P459, G460, T461, V462, T463. The
CC variants can be used for washing and/or dishwashing. They can also be
CC used in the production of sweeteners and ethanol from starch, and/or for
CC textile desizing, and in starch liquefaction and/or saccharification
CC processes. The present sequence encodes an amylase that can function as
CC the parent sequence in the production of the variants of the invention
XX
SQ Sequence 1455 BP; 461 A; 248 C; 361 G; 385 T; 0 U; 0 Other;

Query Match 65.7%; Score 1167; DB 2; Length 1455;
Best Local Similarity 87.6%; Pred. No. 2, 5e-307;
Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

QY 238 CACCAATATGAGACGATGGACCATGATGATTTGAATGAGCATTTGCCAATATGAC 297
DB 1 CACCAATATGAGACGATGGACCATGATGATTTGAATGAGCATTTGCCAATATGAC 60

QY 298 GGGAAACCACTGGAACAGTTTACGAGATGACGAGCTTAACTTAAAGATTAAGGATTTACC 357
DB 61 GGGAAACCACTGGAACAGTTTACGAGATGACGAGCTTAACTTAAAGATTAAGGATTTACC 120
QY 358 GCTGTTGGATTTCTTCCTGCATGGAAGGGGACTTCGCAAAATGATGTTGGTATGTCGCC 417
DB 121 GCTGTTGGATTTCTTCCTGCATGGAAGGGGACTTCGCAAAATGATGTTGGTATGTCGCC 180
QY 418 TATGATTTGATGATCTTGGATGTTTAAACGAAAGGGGACCGTCCGTAACAAATATGCGC 477
DB 181 TATGATTTGATGATCTTGGATGTTTAAACGAAAGGGGACCGTCCGTAACAAATATGCGC 240
QY 478 ACAAGAGTCAGTTGCAAGTCCCGTGCATCTTTGAAATAATACGGGATTCAGTTTAT 537
DB 241 ACAAGAGTCAGTTCAGGCTCGGTAACCTTTTAAATAATACGGGATTCAGTTTAT 300
QY 538 GGGGATGTCGTGATGATCATTAAGGTGAGACAGCGGACAGATGTTAAATGCGGTG 597
DB 301 GGTGATGTCGTGATGATCATTAAGGTGAGACAGCGGATGTTAAATGCGGTG 360
QY 598 GAAGTGAACCGAAGCAACCGAAACCAAGAAATATGAGTGAATACCATGATGATG 657
DB 361 GAAGTGAATCGAGCAACCGAAACCAAGAACTCAGAGATGCAATGATGATGATG 420
QY 658 ACGAAATTTGATTTCCCTGGAAGAGAAATACCAATTCGAACTTTAAATGCGGTGAT 717
DB 421 ACGAAATTTGATTTCCCTGGAAGAGAAATACCAATTCGAACTTTAAATGCGGTGAT 480
QY 718 CATTTGATGAGACAGATTTGGATGATGATGATGATGATGATGATGATGATGATG 777
DB 481 CATTTGATGAGACAGATTTGGATGATGATGATGATGATGATGATGATGATGATG 540
QY 778 AGAGTACCGGAAGGATGAGTGGATGAGTGGATGAGTGGATGAGTGGATGAGTGGATG 837
DB 541 AGAGTACCGGATGAGTGGATGAGTGGATGAGTGGATGAGTGGATGAGTGGATGAT 600
QY 838 CTTATGATGAGACAGATTTGGATGATGATGATGATGATGATGATGATGATGATG 897
DB 601 CTTATGATGAGACAGATTTGGATGATGATGATGATGATGATGATGATGATGATG 660
QY 898 GGAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 957
DB 661 GGAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
QY 958 ATTAATATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTAT 1017
DB 721 ATTAATATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTAT 780
QY 1018 ATGTTGCAAGTTCAGAAATTTGAAAAATGACCTTGCATGCAATCGAAAACTATTAAAT 1077
DB 781 ATGTTGCAAGTTCAGAAATTTGAAAAATGACCTTGCATGCAATCGAAAACTATTAAAT 840
QY 1078 AAAACAAGTTGGAATCATCTCCGTTTCATGTTCTCTTCATTAATTTGTAACAATGCA 1137
DB 841 AAAACAAGTTGGAATCATCTCCGTTTCATGTTCTCTTCATTAATTTGTAACAATGCA 900
QY 1138 TCTAATAGTGGGCTATTTGATATGAGAAATTTTAAATGTTCTGCTGCAAAAA 1197
DB 901 TCTAATAGTGGGCTATTTGATATGAGAAATTTTAAATGTTCTGCTGCAAAAA 960
QY 1198 CACCTATATGAGTCAATCTTTGTTGATTAACATGATCTTCAGCGAGAGAAAGCATTTG 1257
DB 961 CACCTATATGAGTCAATCTTTGTTGATTAACATGATCTTCAGCGCGGAGAGCATTTG 1020
QY 1258 GAATCTTTGTTGATCTGTTGTTCAACATGTCGATGATGATGATTTTGAACAGGAG 1317
DB 1021 GAATCTTTGTTGATCTGTTGTTCAACATGTCGATGATGATGATTTTGAACAGGAG 1080
QY 1318 CAAGTTTACCTTCGTTATTTTACGTTATGATGATGATGATGATGATGATGATGATG 1377
DB 1081 CAAGTTTACCTTCGTTATTTTATGAGGATTTTCTACGTTATGATGATGATGATGATG 1140

QY 1378 TCGATGAATCTAAATGTATGACCTTCTGAGCAGCCTAACGATATGCTTACGAAACC 1437
DB 1141 GCTATGAATCTAAATGTATGACCTTCTGAGCAGCCTTCTTGTCTTATGCTTATGCTACG 1200
QY 1438 CAAATGATTTTATGATCATGATATTTATCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1497
DB 1201 CAGATGATTTATGATCATGATATTTATCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
QY 1498 CACCAATTCAGGACTGCAACTATTTATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1557
DB 1261 CATCAATTCAGGACTGCTTCCACCTTATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
QY 1558 TATGTCGAGAAACATAAGCTGCGCAAGTATGAGAGATATCACCGAATATGCTTGTG 1617
DB 1321 TATGTCGAGAAATTAAGCGGAGCAAGTTTGAAGATATTTACCGAATATGAGACAGGC 1380
QY 1618 ACCGTCACATTAATGACAGATGCTTGGGGAATTTCACTGTAACGAGAGAGAGAGAG 1677
DB 1381 ACCGTCACATTAATGACAGAGATGCGGTATTTCTCTGTTAATGAGAGAGAGAGAGAG 1440
QY 1678 GTTTGGGTGAGCAA 1692
DB 1441 GTTTGGGTGAGCAA 1455

RESULT 9
AAK57597 standard; DNA; 1455 BP.
AAK57597;
XX 16-JUL-1999 (first entry)
DE Wild type Termany1 (RTM)-like alpha-amylase coding sequence #6.
XX Variant; Termany1; alpha-amylase; mutation; Bacillus; detergent;
KM dishwashing; laundry; textile; desizing; starch liquefaction; sweetener;
XX ethanol; ss.
OS Bacillus sp.
PN WO9919467-A1.
XX 22-APR-1999.
PD 13-OCT-1998; 98WO-DK000444.
PF 13-OCT-1998; 98WO-DK000444.
PR 13-OCT-1997; 97DK-00001172.
XX (NOVO) NOVO-NORDISK AS.
PA Svendsen A, Borchert TV, Bisgard-Frantzen H;
XX WPI; 1999-277632/23.
DR
PT Variant alpha-amylases - useful as detergents or for textile desizing or
XX starch liquefaction.
PS Disclosure; Page 83-84; 93pp; English.
XX This sequence represents the coding sequence for a parent sequence used
CC to generate new variants of a Termany1-like alpha-amylase with alpha-
CC amylase activity. The variants comprise mutations in 2-6
CC regions/positions relative to an alpha-amylase from either of two
CC Bacillus species in WO9526397, B. stearothermophilus, B. licheniformis,
CC B. amyloliquefaciens or Bacillus sp. #707. The alpha-amylase variants are
CC detergent additives for use in detergents for dishwashing, manual or
CC automatic laundry. The variants can also be used for textile desizing or
CC starch liquefaction (e.g. for production of sweeteners or ethanol)
XX
SQ Sequence 1455 BP; 461 A; 248 C; 361 G; 385 T; 0 U; 0 Other;
Query March 65.7%; Score 1167; DB 2; Length 1455;

Best Local Similarity 87.6%; Pred. No. 2,5e-307;
Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0;
QY 238 CATCATATGAG 297
DB 1 CATCATATGAG 60
QY 298 GGAACACATGGAACAGATTACAGAGATGACGACAGCTTAATTAAGAGATTAAGAGATTAAC 357
DB 61 GGAATCATTTGGAACAGATTGAGAGATGACGACAGCTTAATTAAGAGATTAAGAGATTAAC 120
QY 358 GCTGTTGAGATTCCTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 417
DB 121 GCTGATGAGATTCACAGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 418 TATGATTTGACATCTTGTGATGATTAACCAAAAGGAGAGAGAGAGAGAGAGAGAGAGAG 477
DB 181 TATGATTTGATATGATCTTGGAGAGATTAACCAAAAGGAGAGAGAGAGAGAGAGAGAGAG 240
QY 478 ACAAGAGTCAGTTGCAAGGTCGTCACATCTTGAATAAATACGGAGATCAAGTTAT 537
DB 241 ACAGGCAACGAGTACAGGCTGCGGTGACCTTTAAATAAATACGGAGATCAAGTTAT 300
QY 538 GGGGATGTCGTGATGAATCAATAAGTGAAGCAGACGAGATGTAATGCGGTG 597
DB 301 GGTGATGTCGTGATGAATCAATAAGTGAAGCAGATGTAATGTAATGCGGTG 360
QY 598 GAATGAAACGAG 657
DB 361 GAATGAAACGAG 420
QY 658 ACGAATTTGATTTCCCTGGAAG 717
DB 421 ACGAATTTGATTTCCCTGGAAG 480
QY 718 CATTTGATGAG 777
DB 481 CATTTGATGAG 540
QY 778 AGAGATACCGGAAG 837
DB 541 AGGGAACAG 600
QY 838 CTTATGATGAG 897
DB 601 CTTATGATGAG 660
QY 898 GGAATTTGATTAACAATTAACAATTAACAATTAACAATTAACAATTAACAATTAACAATTA 957
DB 661 GGAATTTGATTAACAATTAACAATTAACAATTAACAATTAACAATTAACAATTAACAATTA 720
QY 958 ATTAATTAACAATTAACAATTAACAATTAACAATTAACAATTAACAATTAACAATTAACA 1017
DB 721 ATTAATTAACAATTAACAATTAACAATTAACAATTAACAATTAACAATTAACAATTAACA 780
QY 1018 ATGTTTCAGTTCAG 1077
DB 781 ATGTTTCAGTTCAG 840
QY 1078 AAAACAGTTGAGATCACTCCGTTGATGATGATGATGATGATGATGATGATGATGATGAT 1137
DB 841 AAAACAGTTGAGATCACTCCGTTGATGATGATGATGATGATGATGATGATGATGATGAT 900
QY 1138 TCTATATGAGTGGCTATTTGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1197
DB 901 TCTATATGAGTGGCTATTTGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
QY 1198 CACCTTATACATGAG 1257
DB 961 CATCAACACATGCGTTTACCTTTGTTGATTAACCATATATTCAGCCCGGAGAGAGAGAG 1020
QY 1258 GAATCCTTTGTTCAATGCTGGTTCAAAACCACTGGCATATGATGATGATGATGATGATGATG 1317

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Db      1021 GATCCTTTGTTCAACATGTTTAACCACTTGATGATGATTGGTCTGACAAGGSA 1080
QY      1318 CAAGTTTACCTTCGTTATTTTACGGTATCTACGGTAATACCACTCATGTGTTCT 1377
Db      1081 CAAGTTTACCTTCGTTATTTTATGGGATTTACTACGGTAATCCCAACCATGTGTTCG 1140
QY      1378 TCGATGAATCTAAATTTGATTCACCTTCGACAGACGATCAACGATGCTTACGSAAC 1437
Db      1141 GCTATGAATCTAAATTTAGACCTCTTCGACAGACGATCAACCTTTGCTTATGTAAG 1200
QY      1438 CAACATGATTTATTTGATCATCATGATATTTATGCGTGAACGAGAGAGGAGCAGCTCC 1497
Db      1201 CAGCATGATTTACTTTGATCATCATGATATTTATGCGTTGACAGAGAGGAGAAATGACTCC 1260
QY      1498 CACCAATTCAGAGCTTGACATTTATGTCGATGCGGACGAGGGGTATTAATGATG 1557
Db      1261 CATCAAAATTCAGAGCTTGACATTTATGTCGATGCGGATGTCAGATGCTCAAAATGGAATG 1320
QY      1558 TATGTGGGAGAAATTAAGCTGGCAAGTATGAGAGATTCACCGGAAATAGCTGGGT 1617
Db      1321 TATGTGGGAGAAATTAAGCGGAGCAAGTTGAGAGATTTACCGGAAATAGAGACAGGC 1380
QY      1618 ACCGTACCATTTATGTCAGATGTTGGGGAATTTCACTGTAAACGAGGGGCAATTTG 1677
Db      1381 ACCGTACCATTTATGTCAGAGCGATGGGTAATTTCTGTGTTAATGAGAGGTCGTTTCG 1440
QY      1678 GTTTGGGTGAGCAA 1692
Db      1441 GTTTGGGTGAGCAA 1455

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RESULT 10

AAA48480
ID AAA48480 standard; DNA; 1455 BP.

XX AAA48480;

DT 04-SEP-2000 (first entry)

XX Bacillus parent Teramyl-like alpha-amylase DNA sequence #1.

KW Bacillus; alpha-amylase; washing; textile desizing; starch liquefaction;
KM saccharification; muten; mutant; enzyme stability; hybrid; ss.

OS Bacillus sp.

EH Key Location/Qualifiers

FT CDS 1..1455
/*tag= a
/product= "Teramyl-like alpha-amylase"
/partial

FT

XX WO200029560-A1.

XX 25-MAY-2000.

PF 16-NOV-1999; 99WO-DK000628.

PR 16-NOV-1998; 98DK-00001495.

PA (NOVO) NOVO-NORDISK AS.

PI Svendsen A, Kjaerulff S, Bisgard-Frantzen H, Andersen C,

DR WPI; 2000-387777/33.

DR P-PSDB; AAY99602.

XX Variant of parent teramyl-like alpha amylase useful for washing, textile
PT desizing and starch liquefaction, comprising alterations in one or more
XX solvent exposed amino acid residues.

XX Disclosure; Page 65-66; 80pp; English.

CC The present sequence encodes a parent Teramyl-like alpha-amylase from
CC which mutants with increased stability at acidic pH, low calcium
CC concentration and high temperatures have been derived. The sequence was
CC isolated from a Bacillus genomic DNA library. A variant may contain
CC mutations in one or more solvent exposed amino acid residues to increase
CC the overall hydrophobicity of the enzyme or the overall number of methyl
CC groups in the side chains of exposed residues may be increased. The
CC mutations can be incorporated by site-directed mutagenesis or by random
CC mutagenesis. As a result of their increased stability, the variants are
CC suitable for the industrial processing of starch, i.e. starch
CC liquefaction and saccharification. They may also be useful for washing,
CC dishwashing and textile desizing. Hybrid alpha-amylases comprising
CC partial amino acid sequences derived from two or more alpha-amylases have
CC also been created in order to increase enzyme stability

SQ Sequence 1455 BP; 461 A; 248 C; 361 G; 385 T; 0 U; 0 Other;

Query Match 65.7%; Score 1167; DB 3; Length 1455;

Best Local Similarity 87.6%; Pred. No. 2.5e-307;

Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

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QY      238 CATCATATATGGAACGATGGAACCATGATGCAATTTTGAATGGCATTTGCCAAATGAC 297
Db      1 CATCATATATGGAACAAATGCTATGATGCAATATTTGCAATGTAATTTGCCAAATGAC 60
QY      298 GGGAACCACTGGAACAGTTAGAGATGACGAGCTTAATTAAGTAAGTAAGGATTAAC 357
Db      61 GGGAAATCATTTGGAACAGTTAGAGATGACGAGCTTAATTAAGTAAGTAAGGATTAAC 120
QY      358 GCTGTTTGATTCCTCTGTCATGGAAGGGGACTTGCAGAAATGATGTTGGTATGTC 417
Db      121 GCTGATATGATCCACTGTCATGGAAGGGGACTTCCAGAAATGATGATTAAGAGGC 180
QY      418 TATGATTTGATGATTTTGTGAGTTTAAACAAAGGGAACCGTCCGTCAAAATATGCG 477
Db      181 TATGATTTATATGATCTTGTGAGTTTAAACAAAGGGAACCGTCCGTCAAAATATGGA 240
QY      478 ACAAGAGTCAGTTGCAAGTCCGTCATCATCTTTGAAATTAACGGGATTCAGTTTAT 537
Db      241 ACAAGCAACAGTCACAGCTCGGTGACTCTTTAAATTAACGGGATTCAGTTTAT 300
QY      538 GGGGATGTCGTATGATATTAAGGTGAGACAGCGGACAGAGTGTAAATGCGGTG 597
Db      301 GGTGATGTCGTATGATATTAAGGTGAGACAGAGTGTAAATGCGGTG 360
QY      598 GAAATTAACCGAAGCAACCGAATTAATGCGTGAATTAACCTTGAAGCATG 657
Db      361 GAAATTAATCGAAGCAACCGAATTAATGCGTGAAGTGAATTAAGCATG 420
QY      658 ACGAAATTTGATTTCCCTGGAAGAGAAATTAACCATTTCAACTTTAATGGCGTGTAT 717
Db      421 ACGAAATTTGATTTCCCTGGAAGAGAAATTAACCATTTCAAGCTTTAAGTGGCGTGTAT 480
QY      718 CATTTTATGGAACAGATTTGGATGATGATGATGATGATGATGATGATGATGATGATG 777
Db      481 CATTTTATGGAACAGATTTGGATGATGATGATGATGATGATGATGATGATGATGATG 540
QY      778 AGAGTACCGGAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 837
Db      541 AGGGAACAGGACAGGCTGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 600
QY      838 CTTATGATGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 897
Db      601 CTTATGATGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
QY      898 GGAATTTGATTAACAATTAACCTTAATCTAGATGATGATGATGATGATGATGATGAT 957
Db      661 GGAATTTGATTAACAATTAACCTTAATCTAGATGATGATGATGATGATGATGATGATG 720
QY      958 ATTAATTAACGATTAACGAGATTTGGCTTAACATATGTCGTTAACCAACAGTTAAC 1017
Db      721 ATTAATTAATGCTTTAACAAGATTTGGCTTAACATATGTCGTTAACCAACAGTTAAC 780

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QY 1018 ATGTTGACAGTGGAGAAATTTGGAAAAATGACCTGCTGCATCGAAAACTATTAAAT 1077
 DB 781 ATGTTTGAAGTGGAGTGGTGGAAAAATGACCTGGTGGATTTGAAAACTATTGAT 840
 QY 1078 AAAACAAGTTGAATCACTCCGTTGGATGATCTCTTCAATTAATTTGACATGCA 1137
 DB 841 AAAACAAGTTGAATCACTCCGTTGGATGATCTCTTCAATTAATTTGACATGCA 900
 QY 1138 TCTAATGTTGGTGGCTATTTTGTATATGAGAAATATTTAAATGTTCTGTCGTA 1197
 DB 901 TCTAATGTTGGTGGCTATTTTGTATATGAGAAATATTTAAATGTTCTGTCGTA 960
 QY 1198 CACCTTATACATGACATCAATTTGTTGATACCATGACTCTCAGCCAGAGAAATG 1257
 DB 961 CATCAACATGACATCAATTTGTTGATACCATGACTCTCAGCCAGAGAAATG 1020
 QY 1258 GAATCTTTGTTGATGCTGTTGTAACCACTGCGATATGCTATGATTTGCAAGGAG 1317
 DB 1021 GAATCTTTGTTGATGCTGTTGTAACCACTGCGATATGCTATGATTTGCAAGGAG 1080
 QY 1318 CAAAGTTACCTGCTGCTATTTTACGTTGATTAACGCTATACCAATCATGCTGCT 1377
 DB 1081 CAAAGTTACCTGCTGCTATTTTACGTTGATTAACGCTATACCAATCATGCTGCT 1140
 QY 1378 TCGATGAATCTAAATTTGATCACTTCTGACGACAGTCAAAAGTATGCTACGAAAC 1437
 DB 1141 GCTATGAATCTAAATTTGATCACTTCTGACGACAGTCAAAAGTATGCTACGAAAC 1200
 QY 1438 CAACATGATTTATTTGATCATCATGATATTTATGCGCTGACAGAGAAAGGAGAC 1497
 DB 1201 CAGATGATTTATTTGATCATCATGATATTTATGCGCTGACAGAGAAAGGAGAC 1260
 QY 1498 CACCAATTTACAGATTTGACAACTATATGTCGATGCGATGCGAGGGGTAATTAAT 1557
 DB 1261 CACCAATTTACAGATTTGACAACTATATGTCGATGCGATGCGAGGGGTAATTAAT 1330
 QY 1558 TATGTCGAGAAACATTAAGTGTGCGCAAGTATGAGAGATATCACCGAAATAGTCTG 1617
 DB 1321 TATGTCGAGAAACATTAAGTGTGCGCAAGTATGAGAGATATTAACCGAAATAGCA 1380
 QY 1618 ACCGTCAACATTAATGAGATGTTGGGGAATTTCACTGTAAACGAGGAGGAGTT 1677
 DB 1381 ACCGTCAACATTAATGAGATGTTGGGGAATTTCTCTGTAAATGAGGAGGAGTT 1440
 QY 1678 GTTTGGGTGAAGCA 1692
 DB 1441 GTTTGGGTGAAGCA 1455

RESULT 11
 ID AAA48485 standard; DNA; 1455 BP.
 AC AAA48485;

DT 04-SEP-2000 (first entry)
 XX Bacillus Termamyl-like alpha-amylase DNA sequence #3.
 DE Bacillus Termamyl-like alpha-amylase DNA sequence #3.
 XX Bacillus; alpha-amylase; washing; textile desizing; starch liquefaction;
 KM saccharification; mutant; enzyme stability; hybrid; ss.
 XX Bacillus sp.
 OS Bacillus sp.
 FH Key location/Qualifiers
 FT CDS 1.1455
 FT /*tag= a
 FT /product= "Termamyl-like alpha-amylase"
 FT /partial
 PN MO200029560-A1.
 XX 25-MAY-2000.

XX 16-NOV-1999; 99MO-DK000628.
 PF 16-NOV-1998; 98DK-00001495.
 PR (NOVO) NOVO-NORDISK AS.
 PA Svendsen A, Kjaerulf S, Bisgard-Frantzen H, Andersen C;
 PI WPI; 2000-38777/33.
 XX Variant of parent termamyl-like alpha amylase useful for washing, textile
 PT desizing and starch liquefaction, comprising alterations in one or more
 PT solvent exposed amino acid residues.
 XX Disclousure; Page 69-70; 80pp; English.
 PS The present sequence encodes an alpha-amylase from which mutants with
 CC increased stability at acidic pH, low calcium concentration and high
 CC temperatures have been derived. The sequence was isolated from a Bacillus
 CC genomic DNA library. A variant may contain mutations in one or more
 CC solvent exposed amino acid residues to increase the overall
 CC hydrophobicity of the enzyme or the overall number of methyl groups in
 CC the side chains of exposed residues may be increased. The mutations can
 CC be incorporated by site-directed mutagenesis or by random mutagenesis. As
 CC a result of their increased stability, the variants are suitable for the
 CC industrial processing of starch, i.e. starch liquefaction and
 CC saccharification. They may also be useful for washing, dishwashing and
 CC textile desizing. Hybrid alpha-amylases comprising partial amino acid
 CC sequences derived from two or more alpha-amylases have also been created
 CC in order to increase enzyme stability.
 XX Sequence 1455 BP; 461 A; 248 C; 361 G; 385 T; 0 U; 0 Other;
 SQ Query Match 65.7%; Score 1167; DB 3; Length 1455;
 Best Local Similarity 87.6%; Pred. No. 2.5e-307;
 Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0;
 QY 238 CATATATATGAGACGATGAGACCATATGATTTTGAATGATTTGCCAAATGAC 297
 DB 1 CATATATATGAGACGATGAGACCATATGATTTTGAATGATTTGCCAAATGAC 60
 QY 298 GGGAAACACTGGAACAGTTACGAGATGACGACGCTAATTAAGATTAAGGATTAAC 357
 DB 61 GGGAAATATGAGACGATGAGGATGACGACGCTAATTAAGATTAAGGATTAACA 120
 QY 358 GCTGTTGATTTCTCTGATGAGAGGAGACTTGCMAATATGATTTGGGTATGATGCC 417
 DB 121 GCTGTTGATTTCTCTGATGAGAGGAGACTTGCMAATATGATTTGGGTATGAGGCC 180
 QY 418 TATGATTTGATGATCTTGTGATTTAACCAAAAGGAAACCTGCTGCAAAATATGCGC 477
 DB 181 TATGATTTGATGATCTTGTGATTTAACCAAAAGGAAACCTGCTGCAAAATATGCGA 240
 QY 478 ACAAGAGTCAAGTTGCAAGGAGCGGTGACATCTTTGAAAAATTAACGAGATTTCAAT 537
 DB 241 ACAAGAGTCAAGTTGCAAGGAGCGGTGACATCTTTTAAAAATTAACGAGATTTCAAT 300
 QY 538 GGGGATGCTGATGATTAATTAAGGTGAGACGAGACGAGATGATTAATGCGGTG 597
 DB 301 GGTGATGCTGATGATTAATTAAGGTGAGACGAGATGATTAATGCGGTG 360
 QY 598 GAGGTGAACCGAAGCAACCGAAACCAAGAAATATCAGGTGATTAACCATTTGAAGCATGG 657
 DB 361 GAGGTGAATCGAGCAACCGAAACCAAGAAACCTCAGAGAAATATGAAATGAAGCCTGG 420
 QY 658 ACGAAATTTGATTTCCCTGGAAGGAAATACCATTCCTTAATGAGCGTGTAT 717
 DB 421 ACGAAATTTGATTTCCCTGGAAGGAAATACCATTCCTTAATGAGCGTGTAT 480
 QY 718 CATTTGATGAGACAGATTTGGATCACTGACGCTTCAAGACCAAAATATTAATTC 777
 DB 481 CATTTGATGAGACAGATTTGGATCACTGACGCTTCAAGACCAAAATATTAATTC 540

Qy 418 TATGATTGTACGATCTTGTGAGTTTAAACCAAAAGGAAACCGTCCGTAACAAATATGAC 477
 Db 181 TATGATTGTATGATCTTGTGAGATTTAACCAAAAGGAAACCGTCCGTAACAAATATGAG 240
 Qy 478 ACAAGAGTCAGTTGCAAGGTGCGGTGACATCTTTGAAAAATTAACGGGATTCAGATTAT 537
 Db 241 ACAAGCAACAGCTACAGAGGTGCGGTGACCTTTTAAAAATTAACGGGATTCAGATTAT 300
 Qy 538 GGGGATGTCGTGATGATCATTAAGGTGAGACACAGGACAGAGATGTGTAATGCCGTG 597
 Db 301 GGTATGTGCTGATGAATCATTAAGGTGAGACAGATGTGTAATGAATGACGGTA 360
 Qy 598 GAAATGAACCGAAGCAACCGAAACCAAGAAATATCAGTGAATCACCATGGAAGCATGG 657
 Db 361 GAAATGAATCGAGACCAACCGAAACCAAGAAATCTCAGAGAGTTCAGTAATGAAGCGTGG 420
 Qy 658 ACGAAATTTGATTTCCCTGGAAGAGAAATACCCATTCCACTTTAAATGGCGCTGTAT 717
 Db 421 ACAAAATTTGATTTCTCTGGAAGAGAAATTAACCATTCACCTTTAAAGTGGCGGTGAT 480
 Qy 718 CATTTTGTGAGGACAGATGGGATCAGTCAGCTTCAGAACAAATATTAATTC 777
 Db 481 CATTTTGTGAGGACAGATGGGATCAGTCAGCTTCAGAACAAATATTAATTC 540
 Qy 778 AGAGGTACCGGAAAGGACATGGGACATGGAGATAGATTAAGAAACGGCACTATGATTAC 837
 Db 541 AGGGAAACAGGACAGGCTGGGACCTGGGAGTCCATACAGAAATGGCACTTAATGACTAT 600
 Qy 838 CTATATGATGACAGCATTTGATATGATATCAGAAAGTAAATCAATGAAATTTGG 897
 Db 601 CTATATGATGACAGCATTTGATATGATATCAGAAAGTAAATCAATGAAATTTGG 660
 Qy 898 GGAATTTGGTATACAAATACCTTAATCTAGATGATTAATGATGCTGTGAACAT 957
 Db 661 GGAATTTGGTATACAAATACCTTAATCTAGATGATTAATGATGCTGTGAACAT 720
 Qy 958 ATTAAATACAGCTATACAGAGATTTGGCTAACAGATGGCTAACACCAAGGTAAACA 1017
 Db 721 ATTAAATACAGCTATACAGAGATTTGGCTTAACAGATGGCTTAACACCAAGGTAAACA 780
 Qy 1018 ATGTTTCAGTTGACAGATTTTGGAAAAATGACCTTGCAGATTCGAAACCTATTTAAAT 1077
 Db 781 ATGTTTCAGATGAGGTGATGTTTGGAAAAATGACCTTGCAGATTCGAAACCTATTTGAT 840
 Qy 1078 AAAACAAGTTGGAATCACTCCGTGTGATGTTCTCTTCATTAATTTGTAACATGCA 1137
 Db 841 AAAACAAGTTGGAATCACTCCGTGTGATGTTCTCTTCATTAATTTGTAACATGCA 900
 Qy 1138 TCTTAATGCTGTGCTATTTTGTATATGAGAAATATTTAAATGTTCTGTCTGTAACAAA 1197
 Db 901 TCTTAATGCTGTGCTATTTTGTATATGAGAAATATTTAAATGTTCTGTCTGTAACAAA 960
 Qy 1198 CACCTTATACATGACATCACATTTGTTGATACCATGACTCTCAGCCAGAGAAAGCATTTG 1257
 Db 961 CATCAACACATGACCTTACTTTGTTGATACCATGACTCTCAGCCAGAGAAAGCATTTG 1020
 Qy 1258 GAAATCTTTGTTCAATCGTGTGTAACACACTGSCATATGATGATTTCTGACAGGAG 1317
 Db 1021 GAAATCTTTGTTCAATCGTGTGTAACACACTGSCATATGATGATTTCTGACAGGAG 1080
 Qy 1318 CAAGGTTACCTTCCGATATTTTACGGTATATACGTTATACCAACTCATGTTCTTCT 1377
 Db 1081 CAAGGTTATCTTCCGATATTTTACGGGATTAACGTTATACCAACTCATGTTCTTCCG 1140
 Qy 1378 TCGATGAATCTAAATATGATCTCTGAGGACGTCACAAAGTATGCTTACGAAAC 1437
 Db 1441 GCTATGAATCTAAATATGATCTCTTCTGAGGACGTCACAACTTTTGCCTATGATGACG 1200
 Qy 1438 CAACATGATTTATTTGATCATCATGATATTTATCGCTGAGACAGAAAGGGACAGCTCC 1497
 Db 1201 CAGCATGATTTACTTTGATCATCATGATATTTATCGTTGACAAAGAGGAAATAGCTCC 1260

Qy 1498 CACCAAAATTCAGACTTGGCACTATTAATGATGATCCGATGGCCAGGGGTAATAATGATG 1557
 Db 1261 CATCAAAATTCAGGCTTGGCACCATTAATGATGATGATGCTCAGGTGTAACAAATGATG 1320
 Qy 1558 TATGTGGGAAACATAAGCTGGCCCAAGTATGAGAGATATTCACCGAAATAGGTCTGCT 1617
 Db 1321 TATGTGGGAAACATAAGCTGGCCCAAGTATGAGAGATATTCACCGAAATAGGACAGGC 1380
 Qy 1618 ACCGTACCACTTAATGATGATGTTGGGGAAATTTCACTGTAAACGAGAGGGCAGTTTCG 1677
 Db 1381 ACCGTACCAATTAATGATGATGAGATGGGGTAAATTTCTGTATATGAGAGGCTCCGTTTCG 1440
 Qy 1678 GTTTGGGTGAAGCAA 1692
 Db 1441 GTTTGGGTGAAGCAA 1455

RESULT 13
 AAS20022
 ID AAS20022 standard; DNA; 1455 BP.
 XX
 AC AAS20022;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Bacillus DNA encoding TERMAMYL-like alpha-amylose SP690.
 XX
 KW TERMAMYL; alpha-amylose; ds; detergent; dishwashing; textile desizing;
 KW starch liquefaction; ethanol production; hard surface cleaner; sweetener;
 KW amylopectin; limit dextrin; NOVAMYL; SP690.
 OS Bacillus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1455
 FT /*tag= a
 FT /product= "Alpha-amylose SP690"
 FT /partial
 FT /note= "No start or stop codon"
 XX
 XX MO20018107-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 10-MAY-2001; 2001MO-DK000323.
 XX
 PR 12-MAY-2000; 2000DK-00000779.
 XX
 PA (NOVO) NOVOZYMES AS.
 XX
 PI Svendsen A, Jorgensen CT, Nielsen BR;
 XX
 DR WPI; 2002-106123/14.
 DR P-PSDB; AAU12149.
 XX
 PT New variant of parent TermamyL-like alpha-amylose for use as a component
 PT in washing and dishwashing compositions, for textile desizing, for starch
 PT liquefaction, and for producing sweeteners and ethanol from starch.
 XX
 PS Disclosure; Page 42-45; 84pp; English.
 XX
 CC The invention relates to a variant of parent TERMAMYL-like alpha-amylose
 CC comprising an alteration at regions 186-193, 261-276, 283-293 or 334-339,
 CC or at position 234, where the variant has alpha-amylose activity and each
 CC position corresponds to a position of a parent TermamyL-like alpha-
 CC amylose sequence having a Bacillus licheniformis alpha-amylose sequence
 CC of 483 amino acids, given in specification. The variant alpha-amylose, a
 CC detergent additive comprising the variant or a detergent composition
 CC comprising the variant, is useful for washing and/or dishwashing or
 CC textile desizing. The alpha-amylose is useful for starch liquefaction or
 CC ethanol production and as a component in a hard surface cleaning
 CC detergent composition, and for producing sweeteners from starch. The
 CC variant has altered alpha-1, 6-D-glucosidic branch linkage cleavage

CC activity on amylopectin, preferably increased alpha-1, 6-D-glucosidic
 CC branch linkage cleavage activity of amylopectin or a limit dextrin
 CC prepared by TERMAMYL (R)M or NOVAMYL (R)M). The present sequence encodes
 CC a natural variant of the TERMAMYL alpha-amylose, Sp690
 CC
 XX

Sequence 1455 BP; 461 A; 248 C; 361 G; 385 T; 0 U; 0 Other;

Query Match 65.7%; Score 1167; DB 6; Length 1455;
 Best Local Similarity 87.6%; Pred. No. 2.5e-307;
 Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

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QY 238 CATCAATAATGGAGCAGATGGAGCCATGATGAGTATTTGAATGAGCATTTGCCAATGAC 297
DB 1 CATCAATAATGGAGCAGATGGAGCCATGATGAGTATTTGAATGAGCATTTGCCAATGAC 60
QY 298 GGGAGCACTGGAGCAGTTAGAGATGACGAGCTTAACCTTAAGATTAAGGATACC 357
DB 61 GGGAGCACTGGAGCAGTTAGAGATGACGAGCTTAACCTTAAGATTAAGGATTAACA 120
QY 358 GCGTTTGGATTCCCTGATGAGAGGGGACTTGGCAAAATGATGTTGGTATGTTGCC 417
DB 121 GCGTTTGGATTCCCTGATGAGAGGGGACTTCCCAATGATGTTAGTTATGAGGCC 180
QY 418 TATGATTTGATGATCTTGGATGATTTAAACCAAGAGGAAACCGTCCGTACAAATATGAC 477
DB 181 TATGATTTGATGATCTTGGATGATTTAAACCAAGAGGAGCGGTGCTACAAATATGGA 240
QY 478 ACAAGAGATCAGTTGCAAGTGCCTGTCATCTTTGAAATAACGGGATTCAGTTTAT 537
DB 241 ACAAGAGATCAGTTGCAAGTGCCTGTCATCTTTGAAATAACGGGATTCAGTTTAT 300
QY 538 GGGAGTGTGCTGATGATCAATAAGGTGAGCAGAGGAGCAGAGATGTTAAATGCGGTG 597
DB 301 GGGAGTGTGCTGATGATCAATAAGGTGAGCAGAGGAGCAGAGATGTTAAATGCGGTG 360
QY 598 GAAGTGAACCGAAGCAACCGAAACCAAGAAATATCAGTGAATATACCAATTGAAGCATG 657
DB 361 GAAGTGAATCGAGCAACCGAAACCAAGAAACCTCAGAGATGATCAATATGAAAGCGTGG 420
QY 658 AGCAATTTGATTTCCCTGGAAGAGAAATACCATTTCCCACTTTAAATGGCGCTGTAT 717
DB 421 ACMAATTTGATTTCCCTGGAAGAGAAATATACCATTTCCCACTTTAAATGGCGCTGTAT 480
QY 718 CATTTGATGGGACAGATGGGATGATGATGATGATGATGATGATGATGATGATGATGAT 777
DB 481 CATTTGATGGGACAGATGGGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
QY 778 AGAGTACCGGAAGGATGGAATGGAAGTATGATATGAGAAAGGCAATATGATATAC 837
DB 541 AGGGGAACAGGAGGCTGGGATGGAAGTATGATATGAGAAAGGCAATATGATATAC 600
QY 838 CTATATGATGACACATTTGATATGATGATGATGATGATGATGATGATGATGATGAT 897
DB 601 CTATATGATGACACATTTGATATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 898 GGAGTTTGGATCAATATACCTTAATCTAGATGATGATGATGATGATGATGATGATGAT 957
DB 661 GGAGTTTGGATCAATATACCTTAATCTAGATGATGATGATGATGATGATGATGATGAT 720
QY 958 ATTAAATACAGCTATACAGAGATTTGCTTAACATATGATGATGATGATGATGATGAT 1017
DB 721 ATTAAATATATGCTTACAGAGATTTGCTTAACATATGATGATGATGATGATGATGAT 780
QY 1018 ATGTTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1077
DB 781 ATGTTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
QY 1078 AAAACAAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1137
DB 841 AAAACAAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
QY 1138 TCTAATATGTTGCTATTTTGAATGAGAAATATTTTAAATGTTCTGCTGACAAAAA 1197

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DB 901 TCTAATAGCGGTGTTATATGATATGAGAAATATTTTAAATGTTCTGCTGACAAAA 960
QY 1198 CACCTATATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1257
DB 961 CATCAACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
QY 1258 GAATCCTTTGTTCAATCGTGTTCAACACATGATGATGATGATGATGATGATGATGAT 1317
DB 1021 GAATCCTTTGTTCAATCGTGTTCAACACATGATGATGATGATGATGATGATGATGAT 1080
QY 1318 CAAGTTTACCTTCCGTATTTTACGATGATGATGATGATGATGATGATGATGATGAT 1377
DB 1081 CAAGTTTACCTTCCGTATTTTACGATGATGATGATGATGATGATGATGATGATGAT 1140
QY 1378 TCGATGAATCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1437
DB 1141 GCTATGAATCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
QY 1438 CAACATGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1497
DB 1201 CAGCATGATTTACTTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1260
QY 1498 CACCAATTCAGACTTGCAATATATGATGATGATGATGATGATGATGATGATGATG 1557
DB 1261 CATCAAAATTCAGACTTGCAATATATGATGATGATGATGATGATGATGATGATGATG 1320
QY 1558 TATGTCGGGAAACATTAAGCTGGCCAGATGAGAGATATACCGGAAATAGTCTGCT 1617
DB 1321 TATGTCGGGAAACATTAAGCTGGCCAGATGAGAGATATTAACCGGAAATAGGACAG 1380
QY 1618 ACCGTACCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1677
DB 1381 ACCGTACCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440
QY 1678 GTTTGGGTGACCAA 1692
DB 1441 GTTTGGGTGACCAA 1455

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RESULT 14

AA172211
 ID AA172211 standard; cDNA; 1455 BP.

XX AA172211;

DT 02-APR-2002 (first entry)

XX Bacillus alpha amylase sp690 cDNA.

DE Alpha amylase; Bacillus; Termamyl-1-like; maltodextrin; glucose syrup;

KW starch; food; feed; pharmaceutical; confectionery; candy; isotonic drink;

KW bakery; cereal bar; ice cream; coffee whitener; salad dressing;

KW cured meat; fermented meat; spice; ss.

XX Bacillus sp.

OS Key Location/Qualifiers

FT CDS 1.1455

FT /tag= a

FT /note= "No stop codon given"

PD WO200196537-A2.

XX 20-DEC-2001.

XX 13-JUN-2001; 2001WO-DK000404.

XX 14-JUN-2000; 2000DK-0000917.

XX 20-JUN-2000; 2000US-0212852P.

XX (NOVO) NOVOZYMES AS.

XX Nielsen BR, Weibye M;

PI


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OS Bacillus sp.
XX Key Location/Qualifiers
XX CDS 1..1455
FT /tag= a
FT /product= "termyl-like alpha amylase"
FT /partial
FT /note= "no start or stop codon"
XX
XX MO200210355-A2.
XX
XX 07-FEB-2002.
XX
XX 12-JUL-2001, 2001MO-DK000488.
XX
XX 01-AUG-2000, 2000DK-00001160.
XX
XX 12-SEP-2000, 2000DK-00001354.
XX
XX 10-NOV-2000, 2000DK-00001687.
XX
XX 26-APR-2001, 2001DK-00000655.
XX
XX (NOVO ) NOVOZYMES AS.
XX
XX Thisted T, Kjaerulff S, Andersen C, Fuglsang CC;
XX
XX WPI; 2002-280633/32.
XX
XX P-PSDB; ABB76586.
XX
XX Variant of parent Termamy]-like alpha amylase, useful in detergent
XX compositions, for starch liquefaction, ethanol production, washing and/or
XX dish washing, and textile desizing.
XX
XX Disclosure; Page 55-57; 90pp; English.
XX
XX This invention relates to variants of a parent Termamy]-like alpha-
XX amylases. These are used for starch liquefaction, ethanol production,
XX detergent, and textile desizing. The amylases have altered stability,
XX particularly at high temperatures from 70-120plusoc and low pH in the
XX range from pH 4.0-6.0. The present sequence is a termamy]-like-alpha-
XX amylase encoding sequence
XX
XX Sequence 1455 BP; 461 A; 248 C; 361 G; 385 T; 0 U; 0 Other;
XX
XX Query Match 65.7%; Score 1167; DB 6; Length 1455;
XX Best Local Similarity 87.6%; Pred. No. 2.5e-307;
XX Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0;
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XX 1 CATCATTAATGAGCAATGGGACCATGATGAGTATTTGATGCAATGGCAATGGCAATGAC 60
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XX 298 GGGAAACCATGGAACAGGTTACGAGATGACGAGCTTAACCTTAAGATGAAGGATTAAC 357
XX 61 GGGAAACCATGGAACAGGTTACGAGATGACGAGCTTAACCTTAAGATGAAGGATTAAC 120
XX
XX 358 GCTGTTGGATTCCTCGTGAAGAGGAGCTTCCCAAAATGATGTTGGGTATGGTGCC 417
XX 121 GCTGTTGGATTCCTCGTGAAGAGGAGCTTCCCAAAATGATGTTGGGTATGGTGCC 180
XX
XX 418 TATGATTTGATGATCTTGGTGAAGTTTAAACCAAAAGGAAACGCTCGTACAAATATGCG 477
XX 181 TATGATTTGATGATCTTGGTGAAGTTTAAACCAAAAGGAAACGCTCGTACAAATATGCG 240
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XX 478 ACAAGAGTCAGTTGCAAGGTGCGGTGACATCTTTGAAAAATTAACGGATTCAGTTTAT 537
XX 241 ACAAGAGTCAGTTGCAAGGTGCGGTGACATCTTTGAAAAATTAACGGATTCAGTTTAT 300
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XX 538 GGGAGTGTGCTGATGATCATTAAGGTGAGCAGACGAGCAGAGATGTAATGCGGTG 597
XX 301 GGGAGTGTGCTGATGATCATTAAGGTGAGCAGATGTAATGTAATGTAATGCGGTG 360
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XX 598 GAAGTGAACCGAAGCAACCGAAACCAAGAAATATCAGGTGAATATCAACATTTGAAGCATG 657
XX 361 GAAGTGAACCGAAGCAACCGAAACCAAGAAATATCAGGTGAATATCAACATTTGAAGCATG 420

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XX 658 ACGAATTTGATTTCCCTGGAAGAGAAATACCATTCGAATTTAAATGGCGTGTAT 717
XX 421 ACGAATTTGATTTCCCTGGAAGAGAAATACCATTCGAATTTAAATGGCGTGTAT 480
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XX 718 CATTTGATGGAACAGATTGGGATCGATCGCTGAGCTTCAGAACAAATATATTAATTC 777
XX 481 CATTTGATGGAACAGATTGGGATCGATCGCTGAGCTTCAGAACAAATATATTAATTC 540
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XX 1078 AAAACAGTTGGAATACATCGGTGATGATGATGATGATGATGATGATGATGATGATGAT 1137
XX 841 AAAACAGTTGGAATACATCGGTGATGATGATGATGATGATGATGATGATGATGATGAT 900
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XX 1378 TCGATGAATCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1437
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XX 1441 GTTTGGGTGAACAA 1455

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Job time : 676 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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1	1776	100.0	1776	4	US-09-986-676A-1
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3	1170	65.9	1458	2	US-08-600-908A-11
4	1170	65.9	1458	3	US-08-683-838A-11
5	1170	65.9	1458	3	US-09-636-252A-11
6	1167	65.7	1455	1	US-08-446-803-4
7	1167	65.7	1455	2	US-08-861-837-4
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32	927	52.2	1455	3	US-09-170-670-10	Sequence 10, Appl
33	927	52.2	1455	3	US-09-170-670-15	Sequence 15, Appl
34	927	52.2	1455	3	US-09-193-068-14	Sequence 14, Appl
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ALIGNMENTS

RESULT 1
US-09-986-676A-1
; Sequence 1, Application US/09986676A
; Patent No. 6638748
; GENERAL INFORMATION:
; APPLICANT: HATADA, Yuji
; APPLICANT: OZAKI, Katsuya
; APPLICANT: ARA, Katsutoshi
; APPLICANT: KAWAI, Shuji
; APPLICANT: ITO, Susumu
; TITLE OF INVENTION: Gene Encoding Alkaline Liquefying Alpha-Amylase
; FILE REFERENCE: 2173-0121P
; CURRENT APPLICATION NUMBER: US/09/986,676A
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: PCT/JP96/01641
; PRIOR FILING DATE: 1996-06-14
; PRIOR APPLICATION NUMBER: Japan 147257/1995
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1776
; TYPE: DNA
; ORGANISM: Bacillus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (145)..(1692)
; OTHER INFORMATION:
US-09-986-676A-1
Query Match 100.0%; Score 1776; DB 4; Length 1776;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1776; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 ATATTAATTGAATGAACCTATGTAATAATGCTGCGGACGAGAAAAC 60
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QY 301 AACCACTGGAACAGGTTACGAGATGACGAGTAACTTAAGAGATTAAGGATTAACGCT 360
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QY 361 GTTGGATTCCTCTGATGAGAGGGAATTCGCAAAATGATGTTGGGATGATGCTAT 420
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QY 431 GATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 490
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QY 491 AGGAGTCAGTTGCAAGGTCGCGTGAATCTTTGAAAAATTAACGGATTAACGCTTATG 550
QY 541 GATGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
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QY 601 GTGAACCGAAGCAACCGAATATCAAGATGATGATGATGATGATGATGATGATGATGAT 660
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QY 1261 TCCCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
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QY 1321 GGTATCCCTCCGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
QY 1331 GGTATCCCTCCGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1390
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QY 1511 CCAATTTGAGGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1570
QY 1561 GTGCGGAAACATTAAGTGGCCAAATGATGAGATGATGATGATGATGATGATGATGATGAT 1620
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QY 1621 GTCACTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
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QY 1741 CCGATCACTCATACCCCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1776
QY 1751 CCGATCACTCATACCCCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1786

RESULT 3
US-08-600-908A-11
Sequence 11, Application US/08600908A
Patent No. 5989169
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisg rd-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: "Amylase Mutants
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESSES:
ADDRESS: No. 5989169 No. 5989169disk of No. 5989169th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/600,908A
FILING DATE: 13-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

SEO ID NO. 11
LENGTH: 1458
TYPE: DNA
ORGANISM: Bacillus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1455)
US-09-636-252A-11

Query Match 65.9%; Score 1170; DB 3; Length 1458;
Best Local Similarity 87.7%; Pred. No. 0;
Matches 1278; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

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QY 898 GGAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 957
DB 661 GGAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
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QY 1018 ATGTTTGAAGTGAATTTTGAAGAAATGACCTTGTGATGATGATGATGATGAT 1077
DB 781 ATGTTTGAAGTGAATTTTGAAGAAATGACCTTGTGATGATGATGATGATGAT 840
QY 1078 AAAACAAGTTGAATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1137
DB 841 AAAACAAGTTGAATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
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QY 1198 CAACCTATACATGACATGATGATGATGATGATGATGATGATGATGATGATGAT 1257
DB 961 CATCAACATGACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
QY 1258 GAATCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1317
DB 1021 GAATCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
QY 1318 CAAGTTACCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1377
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DB 1201 CAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
QY 1498 CAACCAATTCAGGACTTCACTATGATGATGATGATGATGATGATGATGATGAT 1557
DB 1261 CATCAATTCAGGACTTCACTATGATGATGATGATGATGATGATGATGATGAT 1320
QY 1558 TATGTCGGGAAATTAAGCTGCGCAAGTATGATGATGATGATGATGATGATGAT 1617
DB 1321 TATGTCGGGAAATTAAGCTGCGCAAGTATGATGATGATGATGATGATGATGAT 1380
QY 1618 ACCGTCAACATTAAGCAATGATGATGATGATGATGATGATGATGATGATGAT 1677
DB 1381 ACCGTCAACATTAAGCAATGATGATGATGATGATGATGATGATGATGATGAT 1440
QY 1678 GTTGGGTGAAACAATA 1695
DB 1441 GTTGGGTGAAACAATA 1458
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RESULT 6
US-08-446-803-4
Sequence 4, Application US/08446803
Patent No. 5824531
GENERAL INFORMATION:
APPLICANT: Octrup, Helle
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Ostergaard, Peter Rahbek
APPLICANT: Rasmussen, Michael Dolberg
APPLICANT: Van der Zee, Pia
TITLE OF INVENTION: Alkaline Bacillus Amylase
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: No. 58245310 No. 5824531diak of No. 5824531th America
STREET: 405 Lexington Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,803
FILING DATE: 01-June-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 4157,204-US

```

? TELECOMMUNICATION INFORMATION
? TELEPHONE: (212) 867-0123
? TELEFAX: (212) 878-9655
? INFORMATION FOR SEQ ID NO.: 4:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1455 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? OS=08-446-803-4

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Query Match	65.7%	Score 1167	DB 1	Length 1455
Best Local Similarity	87.6%	Pred. No. 0		
Matches 1275	Conservative	0	Mismatches 180	Indels 0
			Gaps	0

QY	238	TATCATTAATGGAACAATGGGACCAATGACATGATGAGTATTTTGAATGGCATTTGGCAAAATAC	297
Db	1	CATCATTAATGGAACAATGGTATCTATGATGCAATTTTTCGAAATGATATTTGGCAAAATAC	60
QY	298	GGGAACAACCTGGAAACAGGTATACAGATGACCGACGTAACTTTAAAGATPAAAGGATTAC	357
Db	61	GGGAATCATTTGGAAACAGGTATGAGGATGACCGACGTAACTTTAAAGATPAAAGGATTACA	120
QY	358	GCTGTTTGGATTCTCTCTGTCATGGAAGGGGACTTGGCAAAATGATGTTGGGTAATGTGTGCC	417
Db	121	GCTGATGGAATCCCACTGTCATGGAAGGGGAACTTCCAGAAATGATGATGGTTATGGAACCC	180
QY	418	TATGATTTGTAACGATCTTGATGATTTTAAACAAAAGGAAACCGTCCGTACAAAATATGAC	477
Db	181	TATGATTTATATGATCTTGAGAGTTTAAACGAAGGGGACCGTTCCTACAAAATATGGA	240
QY	478	ACAAAGGATCACTTGCAGAGTGCCGTGACATCTTTGAAAAATTAACGGGATTTCAAGTTTAT	537
Db	241	ACAGCGACAACAGCTACAGAGTCCGTGTACTCTTTAAAAAATTAACGGCATTTACGTAATAT	300
QY	538	GGGGATGTCGATGGAATCATPAAAGGTGAGACGACGGGACAGGATGGTAAATCGGATG	597
Db	301	GGTGATGTCTCATGAAATCATPAAAGGTGAGACGATGGTACGAAATTTGTAATTCGGTAA	360
QY	598	GAACTGAAACCGAAGCAACCGAAACCCMAAAATATCAGGTGAAATCACCATTTGAAGCATG	657
Db	361	GAACTGAAATCGAAGCAACCGAAACCGAAACCTCAGAGAGATATGCAATTAAGACGTGG	420
QY	658	ACGAAATTTGATTTTCCCTGGAAAGAGAAATACCATTTCCAATTAAATGGCGCTGTAT	717
Db	421	ACAAAGTTGATTTTCTGGAAAGAGAAATTAACATTCACGTTTAAAGTGGCGCTGTAT	480
QY	718	CATTTGATGGAACAGATTGGGATCAGTCACGTCAGTTCAGAACAAATATTAATTAATTC	777
Db	481	CATTTGATGGAACAGATTGGGATCAGTCACGTCAGTTCAGAACAAATATTAATTAATTC	540
QY	778	AGAGGTACCGGAAAGGCATTTGGGACTGGGAAGTATATAGGAACGGCAACTATGATTAC	837
Db	541	AGGGGAACAGGCAAGGCTCTGGGACTGGGAAGTCGATACAGGAATGGCAACTATGACTAT	600
QY	838	CTTATGATGAGACATTTGATATGGAATCATCCAGAAATTAACAAATTAAGAAATTTGG	897
Db	601	CTTATGATGAGACATTTGATATGGAATCATCCAGAAATTAACAAATTAAGAAATTTGG	660
QY	898	GGAGTTTGGTATACAAATACCTTATATCTAGATGGAATTAGATCGATGCTGTGAAACAT	957
Db	661	GGAGTGTGATATACAAATACCTGAACTTATGATGGAATTAGATCGATGCTGTGAAACAT	720
QY	958	ATTAAATACAGCTATACGAGAGATTGGCTAACACATGTGCGTAAACACACAGGTAAACCA	1017
Db	721	ATTAAATATACCTTTAACGAGAGATTGGCTTACACATGTGCGTAAACACACAGGTAAACCA	780
QY	1018	ATGTTTGACGTGCGAATTTTGGAAAAATGACCTTGCACATCGAATAACATATTAAT	1077
Db	781	ATGTTTGACGTGCGAATTTTGGAAAAATGACCTTGCACATTTGAAATACTATTTGAT	840
QY	1078	AAAAACAGTTGGAATCACTCCGTTGCGATGTTCTCTTCATATATTTGTAACAAATGCA	1137

Db	861	AAAAAAGTTGGATTCACCTGGGTGTTGATGTTCTCTCCACTATATTTGTACATGCA	900
Qy	1138	TCATAAGTGGTGCCTATTTTGTATGAGAAATATTTAAATGGTTCTGTCACAAAA	1197
Db	901	TCTATATAGCGGTGGTTTATGATGATGAGAAATATTTTAAATGGTCTGTGTGTCAAAAA	960
Qy	1198	CACCTTATACATGACATGACATTTGTTGATGATACATGCTCTGACGAGGAAGCATG	1257
Db	961	CATCAACACATGCGCTTACTTGTGTGATACCATATTTCTGACCCCGGGGAAAGCATG	1020
Qy	1258	GAATCCATTTGTTCAATGCTGGTGTCAAAACCATGSCATATGATGATTTCTGACAAGGAG	1317
Db	1021	GAATCCTTTGTTCAACAATGTTTAAACCATGTCATATGATGTTGTTCTGACAAGGGA	1080
Qy	1318	CAAGTTAACCCCTTCGTAATTTTACGGTGAATTACTACGGTATACCAACTCATGTGTTCT	1377
Db	1081	CAAGTTATCCTTCGTAATTTTATGGGGAATTACTACGGTATACCAACCATGTTCTCG	1140
Qy	1378	TCGATGAATTTAAATATGATCCACTTCTGACGACAGTCAAAAGTATGCTTACGGAAC	1437
Db	1141	GCTATGAATTTAAATATGACCCCTTCTGACGACAGTCAAACTTTTGCTTATGTTACG	1200
Qy	1438	CAACATGATTTATTTGATCAATCATGATATTATGCGGTGGAACGAAGAAGGGGACAGCTCC	1497
Db	1201	CAGATGATTTACTTTGATCATCATGATATTTATCGTTGACAAAGAGGAAATAGCTCC	1260
Qy	1498	CACCAAAATTCAGACATTCGCAACTTATATGTCGATGGGCGCAGGGGTAAATAAATGATG	1557
Db	1261	CATCAAAATTCAGGCTCTTGCAACATATATGTCATATGTCAGGTGTGTAACAAATGATG	1320
Qy	1558	TATGTGGGAAACATAAAGCTGCGCAAGTATGAGAGATATCACCGAATATGTTCTGCT	1617
Db	1321	TATGTGGGGAATAATAAGCGGACAAAGTTTGAGAGATTTTACCGGAAATAGACAGGC	1380
Qy	1618	ACCGTCAACATTAATGAGATGTTGGGGGAATTTCACTGTAACGGAAGGGGACGTTTCG	1677
Db	1381	ACCGTCAACATTAATGAGAGAGATGGGTATATTTCTGTTAATGAGAGGTTCCGTTTCG	1440
Qy	1678	GTTTGGGTGAAGCAA 1692	
Db	1441	GTTTGGGTGAAGCAA 1455	
RESULT 7			
US-08-861-837-4			
: Sequence 4, Application US/08861837			
: Patent No. 5856164			
: GENERAL INFORMATION:			
: APPLICANT: Oltup, Helle			
: APPLICANT: Bisgard-Frantzen, Henrik			
: APPLICANT: Ostergaard, Peter Rahbek			
: APPLICANT: Rasmussen, Michael Dolberg			
: APPLICANT: Van Der Zee, Pia			
: TITLE OF INVENTION: Alkaline Bacillus Amylase			
: NUMBER OF SEQUENCES: 5			
: CORRESPONDENCE ADDRESS:			
: ADDRESS: NO. 58561640 No. 5856164disk of No. 5856164th America			
: STREET: 405 Lexington Avenue			
: CITY: New York			
: STATE: New York			
: COUNTRY: USA			
: ZIP: 10174			
: COMPUTER READABLE FORM:			
: MEDIUM TYPE: Floppy disk			
: COMPUTER: IBM PC compatible			
: OPERATING SYSTEM: PC-DOS/MS-DOS			
: SOFTWARE: Patentin Release #1.0, Version #1.25			
: CURRENT APPLICATION DATA:			
: APPLICATION NUMBER: US/08/861,837			
: FILING DATE:			
: CLASSIFICATION: 435			
: PRIOR APPLICATION DATA:			

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1  APPLICATION NUMBER:  US 08/446,803
2  FILING DATE:  01-June-1995
3  ATTORNEY/AGENT INFORMATION:
4
5  NAME:  Harrington, James J.
6  REGISTRATION NUMBER:  38,711
7  REFERENCE/DOCKET NUMBER:  4157.204-US
8
9  TELECOMMUNICATION INFORMATION:
10
11  TELEPHONE:  (212) 867-0123
12  TELEFAX:  (212) 878-9655
13
14  INFORMATION FOR SEQ ID NO:  4:
15
16  SEQUENCE CHARACTERISTICS:
17
18  LENGTH:  1455 base pairs
19
20  TYPE:  nucleic acid
21
22  STRANDEDNESS:  single
23
24  TOPOLOGY:  linear
25
26  MOLECULE TYPE:  DNA (genomic)
27
28  US-08-861-837-4

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Query Match	65.7%	Score 1167	DB 2	Length 1455
Best Local Similarity	87.6%	Pred. No. 0		
Matches 1275; Conservative	0	Mismatches 180	Indels 0	Gaps 0

Oy	238	TATATATA	TGGGAGGAATGGGACCATGATGGAGATT	TTGGAATGGCA	TTTGGCCAAATGAC	297	
Db	1	CATCAATAATGGAA	CAAAATGGTACTATATGCA	ATATTTCCAAATGGTATTTGCCAAATGAC	60		
Oy	298	GGGAACCA	CTGGAA	CAGGTTA	CGAGATGACCGACCTA	CTTAAAGATGAAAGGATTAAC	357
Db	61	GGGAATC	ATTGGAA	CAGGTTAGAGGATGAC	CCAGCTA	CTTAAAGATGAAAGGATTAACA	120
Oy	358	GCTGTTTGGAT	TCTCTCTGCA	TGGAAAGGGGACTTGC	AAATATGATGTTGGGTATGGTGCC	417	
Db	121	GCTGATATGAT	TCCCACTCGCATG	GAAGGGGACTTCCGAAATGATG	TAGGTTATGAGCC	180	
Oy	418	TATGATTTGTA	CGACTTGATGAGTTTA	CCAAAGGAAACCGTCCGTA	CAAAATATGAC	477	
Db	181	TATGATTTATATGAT	CTTGGAAGTTTA	CCGAAGGGGACGTTCTG	TACAAATATGGA	240	
Oy	478	ACAAAGACT	CAGTGGCAAGTGCCGTG	CACTTTGAA	AAATTAACGGGATTCAGATTAT	537	
Db	241	ACAGGCA	CCAGCTACAGGCTGCGGTGAC	CTTTAA	AAATTAACGGCATTCAGATATAT	300	
Oy	538	GGGATGTCGTGAT	TAATCATTAAGTGGAC	CAACGGGACAGATG	GTAAAGCGGTG	597	
Db	301	GGTGATGTCGT	CATGATTAAGGTG	AGAGATGTGAGAAATGT	TAATGACGTA	360	
Oy	598	GAAGGAA	CCGGAAGAACCGAA	CCAA	AAATATCAGGTG	ATAACACATTGAAGACATGG	657
Db	361	GAAGTGAAT	CCGAGCAACCGAA	CCAGAA	ACTTCAGAGATATGCA	TAGAAAGCGTG	420
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Db	421	ACAAATTTG	ATTTTCTTGGAAGAA	ATAATCACTTCAGCTT	TAATGCGCTGTAT	480	
Oy	718	CATTTTGAT	TGGGACAGATTGGGAT	CAATCACA	CGTCA	CGAACAAATATATTAATTC	777
Db	481	CATTTTGA	TGGGACAGATTGGGAT	CAATCACA	CGCTTCAAAACAAATATATTAATTC	540	
Oy	778	AAGGTA	ACCGGAAAGCATGGGACT	GGGAATATAGAA	CGGCAACTATGATTAAC	837	
Db	541	AAGGTA	ACCGGAAAGCATGGGACT	GGGAATATAGAA	ATGCAATATGCAATAT	600	
Oy	838	CTTATGTAT	GCAGACATTTGAT	TGATCAATCCAGAA	GTATCAATGAACTTAGAAATGG	897	
Db	601	CTTATGTAT	GCAGACATTTGAT	TGATCAATCCAGAA	GTATCAATGAACTTAGAAATGG	660	
Oy	898	GGAATTTGGTAT	CAAAATCACTTAATCT	TAAGATGATTTAGAT	TGATGATGCTGTGAAACAT	957	
Db	661	GGAATTTGGTAT	CAAAATCACTTAATCT	TAAGATGATTTAGAT	TGATGATGCTGTGAAACAT	720	
Oy	958	ATTAAAT	TAAAGCTAT	CGAGAGATTTGGCT	TAACAATGTGCTGTA	CAACCAAGGTAAACA	1017
Db	721	ATTAAAT	TAAAGCTAT	CGAGAGATTTGGCT	TAACAATGTGCTGTA	CAACCAAGGTAAACA	780

QY	1018	ATGTTTCAGATGAGAAATTTGGAAAAAAGACCTTGCTCAATCGAAAACTATTTAAAT	107
Db	781	ATGTTTCAGATGCGTGAGTTTGGAAAAAAGACCTTGCTCAATCGAAAACTATTTAAAT	840
QY	1078	AAAAACAAGTTGGAATCACTCCGTTGTGAGATGTTCTCTTCAATATAATTGTCACAAAGCA	1137
Db	841	AAAAACAAGTTGGAATCACTCCGTTGTGAGATGTTCTCTTCAATATAATTGTCACAAAGCA	900
QY	1138	TCTAATAGTGGTGCCTATTTTGTATGAGAAATTTTAAATGGTTCGTGTAACAAAA	1197
Db	901	TCTAATAGTGGTGCCTATTTTGTATGAGAAATTTTAAATGGTTCGTGTAACAAAA	960
QY	1198	CACCCATACATGCAATCACTTGTGTTGATTAACCATGACTCTCAGCCAGAGAAAGCATGG	1257
Db	961	CATCCAAACACATGCGCTGTAATCTTTGTTGATTAACCATATTTCTCAGCCCGGGGAAAGCATGG	1020
QY	1258	GAATCCCTTGGTCAATGCGTGGTCAAAACACTGSCATATGATGATTCGTGACAAAGGAG	1317
Db	1021	GAATCCCTTGGTCAACAAATGGTTTAAACCACTTGATGATTCGTGACAAAGGAG	1080
QY	1318	CAAGTTACCCCTTCGGATATTTTACGGTGATTACTACGGTATACCAACTCATGTGTTCTCT	1377
Db	1081	CAAGTTATCTTCGGATATTTTACGGGATTTACTACGGTATCTCCAAACCAATGAGTGTTCGG	1140
QY	1378	TGATGAAATCTAAATTTGATTCACCTCTGAGGCAAGTCAAAAGTATGCTTACGCAAC	1437
Db	1141	GCTATGAAATCTAAATTTGATTCACCTCTTGGAGGCAAGTCAAACTTTTGCTTATGCTAGC	1200
QY	1438	CAACATGATTTATTTTGAATCATCATGATATTAATTCGGCTGAGCAGAGAAAGGGAACACTCC	1497
Db	1201	CAGCATGATTTACTTTGATCATCATGATATTAATTCGGTGTGACAAAGAGGGGAAATGCTCC	1268
QY	1498	CACCCAAATTCAGACATTCGCAACTTATATGTCCTGAGGCAAGGGGGGTAAATAATGATG	1557
Db	1261	CATCCAAATTCAGGCTTGCCACCACTTAATGTCAGATGCTCCAGGTGGTAAACAAATGATG	1320
QY	1558	TATGTCGGGAAACATAAAGCTGGCCAAATGATGAGAGATATCACCGAATAATAGTCTTGGT	1617
Db	1321	TATGTCGGGAAAAAATAAAGCCGGAACAAATTTGAGAGATATTAACCGGAAATAGGACAAGC	1380
QY	1618	ACCGTACCATTAAATGCAATGATGTTGGGGGAATTTCACTGTAAACGAGGGGCAAGTTTGG	1677
Db	1381	ACCGTACCAATTAATGACAGCAGGATGGGTAAATTTCTGTAAATGAGGGGTCTTTCG	1440
QY	1678	GTTTGGGTGAAGCAA 1692	
Db	1441	GTTTGGGTGAAGCAA 1455	

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? RESULT 8
? US-08-600-656-4
? Sequence 4, Application US/08600656
? Patent No. 6093562
?
? GENERAL INFORMATION:
?
? APPLICANT: Bisgaard-Frantzen, Henrik
? APPLICANT: Svendsen, Allan
? APPLICANT: Borcherdt, Torben Vedel
? TITLE OF INVENTION: AMYLASE VARIANTS
? NUMBER OF SEQUENCES: 32
? CORRESPONDENCE ADDRESSES:
? ADDRESSSEE: No. 60935620 No. 6093562disk of No. 6093562th America, Inc
? STREET: 405 Lexington Avenue, Suite 6400
? CITY: New York
? STATE: New York
? COUNTRY: U.S.A.
? ZIP: 10174-6401
?
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
? CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/08/600,656
FILING DATE: 13-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4318.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1455 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-600-656-4

Query Match 65.7% Score 1167; DB 3; Length 1455;
Best Local Similarity 87.6%; Pred. No. 0; Mismatches 180; Indels 0; Gaps 0;
Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

QY 238 CATCATATGAGAGATGGAGACCATGATGAGATTTTGAATGGCATTTGCCAATATAC 297
DB 1 CATCATATGAGAGACCATGATGAGATTTTGAATGGCATTTGCCAATATAC 60
QY 298 GGGAAACCTGGAACAGTTACAGAGATACCGAGCTTAATTAAAGATTAAGGATTACC 357
DB 61 GGGAAATCTTGGAAACAGTTACAGAGATACCGAGCTTAATTAAAGATTAAGGATTACA 120
QY 358 GCTGTTGGATTCTCCTCGATGAGAGGGGACTTCGCAAAATGATGGGTATGATGCC 417
DB 121 GCTGTTAGATCCACCTCGATGAGAGGGGACTTCGCAAAATGATGGGTATGAGACC 180
QY 418 TATGATTTGATGATCTTGTGATTTTAACCAAAAGGAAACGTCCTGACAAATATGAC 477
DB 181 TATGATTTGATGATCTTGTGATTTTAACCAAAAGGAAACGTCCTGACAAATATGAG 240
QY 478 ACAGAGATCAGTTGCAAGGTGCGCTGACATCTTTGAAAAATTAACGGATTCAGATTAT 537
DB 241 ACAGCAACCAAGCTACAGGTGCGCTGACATCTTTAAAAATTAACGGATTCAGATTAT 300
QY 538 GGGGATGCGTGAATCATTAAGTGGAGACGAGACGAGATGATTAATGCGGTG 597
DB 301 GGTATGTCGTCATGAATCATTAAGTGGAGACGAGATGATTAATGCGGTG 360
QY 598 GAACTGAACCGAAGCAACCAAGAAATATCATGATTAACCATTTGAAGCATGG 657
DB 361 GAACTGAATCGAGCAACCGAAGCAACCAAGAAATATCATGATTAACCATTTGAAGCAT 420
QY 658 ACGAAATTTGATTTCTCTGGAAGAGAAATACCATTTCAACTTTAAATGGCGCTGAT 717
DB 421 ACGAAATTTGATTTCTCTGGAAGAGAAATACCATTTCAACTTTAAATGGCGCTGAT 480
QY 718 CATTTGATGGAGAGATTTGGGATCAGTCACTGACCTTGCAACAAATATATTAATTC 777
DB 481 CATTTGATGGAGAGATTTGGGATCAGTCACTGACCTTGCAACAAATATATTAATTC 540
QY 778 AGAGATCCGGAAGAGATGGGATGGGAGATGATAGAGAAACGCACTATGATTAC 837
DB 541 AGGGAACAGGCAAGGCTGGGATCTGGGAATCGATACAGAAATGCAATATGACAT 600
QY 838 CTATGATGACAGATTTGATGATGATCATCAAGATTAATCAATGAATGAATGG 897
DB 601 CTATGATGACAGATTTGATGATGATCATCAAGATTAATCAATGAATGAATGG 660
QY 898 GGAATTTGATTAAGAAATACCTTAATGATGATTTAATGATGATGATGATGAT 957
DB 661 GGAATTTGATTAAGAAATACCTTAATGATGATTTAATGATGATGATGATGAT 720
QY 958 ATTAATACAGCTATACAGAGATTTGGCTAACATGTCCTTAACACCAAGTAAACA 1017

DB 721 ATAAATATAGCTTTACAGAGATTTGGCTTACATGTCGTGAACACCAAGATTAACA 780
QY 1018 ATGTTGAGATTCAGAAATTTTGGAAAAATGACCTTGTGCAATGAAATCTATTAAT 1077
DB 781 ATGTTGAGATTCAGAAATTTTGGAAAAATGACCTTGTGCAATGAAATCTATTAAT 840
QY 1078 AAAACAAGTGAATCACTCCGTTGATGATGATGATGATGATGATGATGATGATGAT 1137
DB 841 AAAACAAGTGAATCACTCCGTTGATGATGATGATGATGATGATGATGATGATGAT 900
QY 1138 TCTAATAGTGTGCTATTTTGAATAGAAATATTTTAAATGTTCTGTGTGCAAAA 1197
DB 901 TCTAATAGTGTGCTATTTTGAATAGAAATATTTTAAATGTTCTGTGTGCAAAA 960
QY 1198 CACCTATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1257
DB 961 CACCTATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
QY 1258 GAATCCTTTGTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1317
DB 1021 GAATCCTTTGTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
QY 1318 CAAGTTACCTTCGATATTTTACGATGATGATGATGATGATGATGATGATGATGAT 1377
DB 1081 CAAGTTACCTTCGATATTTTACGATGATGATGATGATGATGATGATGATGATGAT 1140
QY 1378 TCGATGAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1437
DB 1141 TCGATGAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
QY 1438 CAACATGATTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1497
DB 1201 CAGATGATTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
QY 1498 CACCAATTTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1557
DB 1261 CATCAATTTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
QY 1558 TATGTCGGAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1617
DB 1321 TATGTCGGAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
QY 1618 ACCGTCACATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1677
DB 1381 ACCGTCACATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
QY 1678 GTTGGGTGAGCA 1692
DB 1441 GTTGGGTGAGCA 1455

RESULT 9
US-09-170-670-9
Sequence 9, Application US/09170670
Patent No. 6187526
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Bisgaard-Frantzen Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 5276, 200-US
CURRENT APPLICATION NUMBER: US/09/170,670
CURRENT FILING DATE: 1998-10-13
EARLIER FILING DATE: 1997-10-13
EARLIER APPLICATION NUMBER: 60/063,306
EARLIER FILING DATE: 1997-10-28
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 1455
TYPE: DNA
ORGANISM: Bacillus sp.

US-09-170-670-9

Query Match 65.7%; Score 1167; DB 3; Length 1455;
 Best Local Similarity 87.6%; Pred. No. 0;
 Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

238 CATCATATATGGAAGAAATGGGACCATGATGAGTATTTGATGATGCAATTTGCCAAATGAC 297
 1 CATCATATATGGAAGAAATGGGACCATGATGAGTATTTGATGATGCAATTTGCCAAATGAC 60
 298 GGAACCACTGGAAACAGTTAGAGATGAGCGAGCTTAAGTAAAGATAAGGATTAAC 357
 61 GGAATCATTTGAAACAGTTAGAGATGAGCGAGCTTAAGTAAAGATAAGGATTAAC 120
 358 GCTGTTGATTCCTCTCGATGGAAGGGGACTTCGAAAATGATGTTGGTATGTC 417
 121 GCTGATGATTCCTCGATGGAAGGGGACTTCGAAAATGATGTTGGTATGTC 180
 418 TATGATTTGATGATCTTGGTATGATTAACCAAAAGGAAACCGTCCGTAACAAATATGAC 477
 181 TATGATTTGATGATCTTGGTATGATTAACCAAAAGGAAACCGTCCGTAACAAATATGAC 240
 478 ACAAGAGTATGATGGAAGGTCGATGATGATGATGATGATGATGATGATGATGATGAT 537
 241 ACAAGAGTATGATGGAAGGTCGATGATGATGATGATGATGATGATGATGATGATGAT 300
 538 GGGGATGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 597
 301 GGTGATGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
 598 GAAATGAAACGGAAGCAACCGAAACCAAAATATGATGATGATGATGATGATGATGATG 657
 361 GAAATGAAACGGAAGCAACCGAAACCAAAATATGATGATGATGATGATGATGATGATG 420
 658 ACGAAATTTGATTTCCCTGGAAGGAAATACCATTCCTCAATTTAATGCGCTGAT 717
 421 ACGAAATTTGATTTCCCTGGAAGGAAATACCATTCCTCAATTTAATGCGCTGAT 480
 718 CATTTGATGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 777
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 778 AGAGATCCGGAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 837
 541 AGGGAACAGGCAAGGCTGGAAGTGAATGATGATGATGATGATGATGATGATGATGAT 600
 838 CTTATGATGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 897
 601 CTTATGATGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
 898 GGAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 957
 661 GGAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
 958 ATTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1017
 721 ATTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
 1018 ATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1077
 781 ATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
 1078 AAAACAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1137
 841 AAAACAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
 1138 TCTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1197
 901 TCTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
 1198 CACCTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1257
 961 CATCAACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020

1258 GAATCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1317
 1021 GAATCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
 1318 CAAGTTACCTTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1377
 1081 CAAGTTACCTTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
 1378 TCGATGAAATCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1437
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 1438 CAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1497
 1201 CAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
 1498 CACCAATTCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1557
 1261 CATCAATTCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
 1558 TATGTCGGAACATTAAGTCTGCAAGTATGATGATGATGATGATGATGATGATGATG 1617
 1321 TATGTCGGAACATTAAGTCTGCAAGTATGATGATGATGATGATGATGATGATGATG 1380
 1618 ACCGTACCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1677
 1381 ACCGTACCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440
 1678 GTTGGTGAAGCA 1692
 1441 GTTGGTGAAGCA 1455

RESULT 10
 US-09-170-670-14
 ; Sequence 14, Application US/09170670
 ; Patent No. 6187576
 ; GENERAL INFORMATION:
 ; APPLICANT: Svendsen, Allan
 ; APPLICANT: Borchert, Torben
 ; APPLICANT: Biegaard-Frantzen Henrik
 ; TITLE OF INVENTION: Alpha-Amylase Mutants
 ; FILE REFERENCE: 5276-200-US
 ; CURRENT APPLICATION NUMBER: US/09/170,670
 ; EARLIER FILING DATE: 1998-10-13
 ; EARLIER APPLICATION NUMBER: 1172/97
 ; EARLIER FILING DATE: 1997-10-13
 ; EARLIER APPLICATION NUMBER: 60/063,306
 ; EARLIER FILING DATE: 1997-10-28
 ; NUMBER OF SEQ. ID NOS: 22
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 14
 ; LENGTH: 1455
 ; TYPE: DNA
 ; ORGANISM: Bacillus sp.
 US-09-170-670-14

Query Match 65.7%; Score 1167; DB 3; Length 1455;
 Best Local Similarity 87.6%; Pred. No. 0;
 Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

238 CATCATATATGGAAGAAATGGGACCATGATGAGTATTTGATGATGCAATTTGCCAAATGAC 297
 1 CATCATATATGGAAGAAATGGGACCATGATGAGTATTTGATGATGCAATTTGCCAAATGAC 60
 298 GGAACCACTGGAAACAGTTAGAGATGAGCGAGCTTAAGTAAAGATAAGGATTAAC 357
 61 GGAATCATTTGAAACAGTTAGAGATGAGCGAGCTTAAGTAAAGATAAGGATTAAC 120
 358 GCTGTTGATTCCTCTCGATGGAAGGGGACTTCGAAAATGATGTTGGTATGTC 417
 121 GCTGATGATTCCTCGATGGAAGGGGACTTCGAAAATGATGTTGGTATGTC 180

QY	718	CATTTGATGGACAGATTGGGATCAGTCAGTCAAGCTTCAGAACCAAAATATATAATTC	777
Db	481	CATTTGATGGGACAGATTGGGATCAGTCAGTCAGCTTCAGAACCAAAATATATAATTC	540
QY	778	AGAGGTACCGAAAGCGATGGGACTGGAGTGAATATAGAAACGGCACTATGATTAC	837
Db	541	AGGGGAACAGGCAAGGCTCGGACCTGGAGATGCGATACAGGAATGCGCACTATGACTAT	600
QY	838	CTTATGTATGACACATGATATGGATCATCCAGAAATCAATGAACTTAGAAATGG	897
Db	601	CTTATGTATGACAGCTGGATATGGATCAACCAGAAATATACATGAACTTAGAAACCTGG	660
QY	898	GGAGTTTGGTATACAAATACCTTATCTAATGGATTTAGAAATCATGATGCTGTGAACAT	957
Db	661	GGAGTGTGGTATACGAATACCTGAACTTATGATTTAGAAATGAGATGCAAGTGAACAT	720
QY	958	ATTAAATACACTATACAGAGATTTGGCTAACACATGTGCGCTAACACACAGAGTAAACA	1017
Db	721	ATTAAATATACCTTTACAGAGATTTGGCTTACACATGTGCGTAAACACAGATTAACCA	780
QY	1018	ATGTTTGCAGTTGCAGAAATTTTGGAAAAATGACCTTGCTGCATGAACTAATTTAAT	1077
Db	781	ATGTTTGCAGTGGCTGAGTTTGGAAAAATGACCTTGCTGCATGAACTAATTTGAAAT	840
QY	1078	AAAACAAGTTGGAATCACTCGGTGTGCAATGTTCTCTCAATTTAATTTGTAACAATCA	1137
Db	841	AAAACAAGTTGGAATCACTCGGTGTGTAATGTTCTCTCACTAATTTTGTACATATCA	900
QY	1138	TCTAATAGTGTGCTATTTTGTATATGAAATAATTTTAAATGTTCTGTGTCACAAAA	1197
Db	901	TCTAATAGCGGTGTTATATGATATGAAATAATTTTAAATGTTCTGTGTGCAAAAA	960
QY	1198	CACCTATACATGACATGACATTTTGTATATACATGCTCGACCGCAGGAAGACATTC	1257
Db	961	CATCCAAACATGCGCTTACTTTTGTATATCAATGATCTCAGCCCGGGAAAGCATTC	1022
QY	1258	GAAATCTTTGTTCAATCGTGTGTCAAAACCACTGCGATATGCAATGATTTCTGACAAAGGAG	1317
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QY	1318	CAAGTTTACCTTCGATTTTAAACGGTATTAACAGGTATTAACCAATCATATGATGTTCT	1377
Db	1081	CAAGTTTATCTTCGATTTTAAACGGGATTAACAGGTATTAACCAATCATATGATGTTCT	1140
QY	1378	TCGATGAATCTAAATATGATTCATTGTCAGGACGCTCAAAACGTATGCTTACGGAACC	1437
Db	1141	GCTATGAATCTAAATATGACCTCTTCTGCAAGGACGCTCAAACTTTTGCTTATGTATGACG	1200
QY	1438	CAATATGATTTTGTATCATCATGATATTAATCGGCTGACAGAGAAAGGGGACAGCTTC	1497
Db	1201	CAGATGTATTTCTTGATCATCATGATATTAATCGGTTGACAGAGAAAGGGGAAATGCTTC	1260
QY	1498	CACCAAAATTCAGGACTTGCAACTATTAATGTCCGATGGGCCAGGGGGGTATTAATGATATG	1557
Db	1261	CATCCAAATTCAGGCTTGCACCATTAATGTCAATGTGTCACAGGTGATTAACAAATGATATG	1320
QY	1558	TATATTCGGGAAACATTAAGCTGCGCAAGTATGAGAGATATCAACCGGAAATATGATCTGTGT	1617
Db	1321	TATATTCGGGAAAAATTAAGCGGAGCAAAATTTGAGAGATATTAATTCGGAATATGACACAGGC	1380
QY	1618	ACCCTCAACATTAATGACATGATGTTGGGGGAATTTCACTGTAAACGAGGGGGCAGTTTCG	1677
Db	1381	ACCCTCAACATTAATGACAGAGGATGGGGTATTTCTCTGTAAATGAGGGGTGCGTTTCG	1440
QY	1678	GTTTGGGTGAAGCAA 1692	
Db	1441	GTTTGGGTGAAGCAA 1455	

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; Patent No.6197565
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Kjirulff, S ren
; APPLICANT: Bisgaard-Frantzen, Henrik
; TITLE OF INVENTION: -Amylase Variants
; FILE REFERENCE: 5709.000-US
; CURRENT APPLICATION NUMBER: US/09/193,068
; CURRENT FILING DATE: 1998-11-16
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Bacillus sp.
US-09-193-068-13

Query Match          65.7%   Score 1167;  DB 3;  Length 1455;
Best Local Similarity 87.6%   Pred. No. 0;
Matches 1275;  Conservative 0;  Mismatches 180;  Indels 0;  Gaps 0;

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QY 1018 ATGTTGAGTTGAGAAATTTTGGAAAAATGACCTTGCTGAGAAAGAACTATTAAAT 1077
 DB 781 ATGTTGAGAGTGGCTGAGATTTTGGAAAAATGACCTTGCTGAGAAAGAACTATTAAAT 840
 QY 1078 AAAACAAGTTGGAATCACTCCGTTGTCAGATGTTCTCTTCAATTAATTTTGAACATCA 1137
 DB 841 AAAACAAGTTGGAATCACTCCGTTGTCAGATGTTCTCTTCAATTAATTTTGAACATCA 900
 QY 1138 TCTAATAGTGGTGTATTTTGAATGAGAAATTTTAAATGTTCTGTCGTACAAAA 1197
 DB 901 TCTAATAGTGGTGTATTTTGAATGAGAAATTTTAAATGTTCTGTCGTACAAAA 960
 QY 1198 CACCTTATACATGAGTACATTTGTTGATACCACTCTCAGCCGCGAGAAAGCATG 1257
 DB 961 CATCAACACATGCGCTTACTTTGTTGATACCACTCTCAGCCGCGAGAAAGCATG 1020
 QY 1258 GAATCCTTTGTTCAATCGTGTTCAAACCACTGCGATATGATTTCTGACAGAGG 1317
 DB 1021 GAATCCTTTGTTCAATCGTGTTCAAACCACTGCGATATGATTTCTGACAGAGG 1080
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 DB 1081 CAAGTTACCTTCCTGATTTTAAAGGTATTAATACTGATATCACTGATGTTCT 1140
 QY 1378 TCGATGAAATGATAATGATCACTCTGAGAGGACCTCAAGCATGCTTACAGAAC 1437
 DB 1141 GCTATGAAATGATAATGATCACTCTGAGAGGACCTCAAGCATGCTTACAGAAC 1200
 QY 1438 CAACATGATTTTATGATCATGATATTAATCGGCTGAGAGAGAGAGAGAGAGAG 1497
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 QY 1498 CACCAATTCAGACCTTGCACTTATTAATGTCAGATGAGGAGAGAGAGAGAGAG 1557
 DB 1261 CATCAATTCAGACCTTGCACTTATTAATGTCAGATGAGGAGAGAGAGAGAGAG 1320
 QY 1558 TATGCGGAGAAACATAAGCTGCGCAAGTATGAGAGATATCACCGGAAATGCTGCT 1617
 DB 1321 TATGCGGAGAAATTAAGCTGCGCAAGTATGAGAGATATTAATCACCGGAAATGCTGCT 1380
 QY 1618 ACCGTCAACATTAATGAGATGTTGGGAGATTTCACTGTAACGAGAGAGAGAGAG 1677
 DB 1381 ACCGTCAACATTAATGAGATGTTGGGAGATTTCTCTGTAATGAGAGAGAGAGAG 1440
 QY 1678 GTTGGGTGAAGCA 1692
 DB 1441 GTTGGGTGAAGCA 1455
 RESULT 13
 US-09-183-412-9
 ; Sequence 9, Application US/09183412
 ; Patent No. 6204232
 ; GENERAL INFORMATION:
 ; APPLICANT: Borchert, Torben V.
 ; APPLICANT: Svendsen, Allan
 ; APPLICANT: Andersen, Carsten
 ; APPLICANT: Nielsen, Bjarne
 ; APPLICANT: Nielsen, Torben L.
 ; APPLICANT: Kjaerulf, Soren
 ; TITLE OF INVENTION: Alpha-Amylase Mutants
 ; FILE REFERENCE: 5368.200-US
 ; CURRENT APPLICATION NUMBER: US/09/183,412
 ; CURRENT FILING DATE: 1998-10-30
 ; EARLIER APPLICATION NUMBER: 60/064,662
 ; EARLIER FILING DATE: 1997-11-06
 ; EARLIER APPLICATION NUMBER: 60/093,234
 ; EARLIER FILING DATE: 1998-07-17
 ; EARLIER APPLICATION NUMBER: 1240/97
 ; EARLIER FILING DATE: 1997-10-30
 ; EARLIER APPLICATION NUMBER: PA 1998 00936
 ; EARLIER FILING DATE: 1998-07-14

NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO: 9
 ; LENGTH: 1455
 ; TYPE: DNA
 ; ORGANISM: Bacillus
 US-09-183-412-9
 Query Match 65.74; Score 1167; DB 3; Length 1455;
 Best Local Similarity 87.6%; Pred. No. 0;
 Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0;
 QY 238 CATCATATGAGAGAAATGAGACCATGATGAGATTTTGAATGAGAGATTTGCAATATAC 297
 DB 1 CATCATATGAGAGAAATGAGACCATGATGAGATTTTGAATGAGAGATTTGCAATATAC 60
 QY 298 GGAAGCACTGGAACAGGTTACGAGATGACCGACATTAATTAAAGATTAAGGATTAAC 357
 DB 61 GGAATCATTTGGAACAGGTTAGGAGATGACCGACATTAATTAAAGATTAAGGATTAAC 120
 QY 358 GCTGTTGAGATTCCTCTGATGAGAGAGGACCTTCCGAAATGATTTGGTATGTC 417
 DB 121 GCTGATGAGATCCACCTGATGAGAGAGGACCTTCCGAAATGATTTGATGAGAGCC 180
 QY 418 TATGATTTGATGATCTTGTGATTTTAAACCAAGGAAACCGTCCGATCAAAATATG 477
 DB 181 TATGATTTGATGATCTTGTGATTTTAAACCAAGGAAACCGTCCGATCAAAATATG 240
 QY 478 ACAAGAGTCAAGTTCAGAGGTCGCTGATCTTTGAAAAATACGGGATTCAGATTAT 537
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 QY 538 GGGATGCTGATGATATCATTAAGGTGAGACAGAGCGGACAGAGATGTAATGCGGTG 597
 DB 301 GGTATGCTGATGATATCATTAAGGTGAGACAGAGCGGATGTAATGTAATGCGGTA 360
 QY 598 GAATGAAACGGAACCAACCGAAATCAAGAAATATCAGTGAATACCATGAAAGCATG 657
 DB 361 GAATGAAATCGAACAACCGAAACCAAGAAATATCAGTGAATACCATGAAAGCATG 420
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 DB 421 ACGAAATTTGATTTCCCTGGAAGAGAAATACCATTCATTAATGAGCGCTGAT 480
 QY 718 CATTTGATGAGACAGATTTGGATCAGTCACTGAGCTTCAAGAACAAATATTAATTC 777
 DB 481 CATTTGATGAGACAGATTTGGATCAGTCACTGAGCTTCAAGAACAAATATTAATTC 540
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 DB 601 CTATGATGAGACATTTGATGATGATCATCAGAAATTAATCAATGAACTTAATTAAT 660
 QY 898 GAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 957
 DB 661 GAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
 QY 958 ATTAAATGAGCTTATGAGAGATGGAATGGAATGGAATGGAATGGAATGGAATGGAAT 1017
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Db 901 TCTAAATAGCGGTGTTATATGATATGAGAAATATTTTAAATGTTCTGTGGGCAAAA 960
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Db 961 CATCCACACATGCGCTTACTTTTGTGATTAACCATGATTTCTAGCCCGGAGAGCATTTG 1020
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QY 1378 TCGATGAATCTAAATTTGATTCACCTTCTGACGACATGCAACGATATGCTTA 1437
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QY 1618 ACCGTCAACATTTATGCAATGTTGGGGGAATTTCACTGTTAAACGAGAGGCGCATTTG 1677
Db 1381 ACCGTCAACATTTATGCAAGAGAGAGATGAGATTTCTGTTAAAGAGGATCGGTTTCG 1440
QY 1678 GTTGGGTGAAGCAA 1692
Db 1441 GTTGGGTGAAGCAA 1455

RESULT 14

US-09-183-412-13
Sequence 13, Application US/09183412

Patent No. 6204332

GENERAL INFORMATION:

APPLICANT: Borchert, Torben V.

APPLICANT: Svendsen, Allan

APPLICANT: Nielsen, Carsten

APPLICANT: Nielsen, Bjarne

APPLICANT: Nielsen, Torben L.

TITLE OF INVENTION: Alpha-Amylase Mutants

FILE REFERENCE: 5368.200-US

CURRENT APPLICATION NUMBER: US/09/183,412

EARLIER APPLICATION NUMBER: 60/064,662

EARLIER FILING DATE: 1997-11-06

EARLIER APPLICATION NUMBER: 60/093,234

EARLIER FILING DATE: 1998-07-17

EARLIER APPLICATION NUMBER: 1240/97

EARLIER FILING DATE: 1997-10-30

EARLIER APPLICATION NUMBER: PA 1998 00936

EARLIER FILING DATE: 1998-07-14

NUMBER OF SEQ ID NOS: 58

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 13

LENGTH: 1455

TYPE: DNA

ORGANISM: Bacillus sp.

US-09-183-412-13

Query Match 65.7%; Score 1167; DB 3; Length 1455;
Best Local Similarity 87.6%; Pred. No. 0;

Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0;
QY 238 CATCTAATGGGACCAATGGGACCATGATGAGTATTTGATGGCATTTGCCAAATATAC 297
Db 1 CATCTAATGGGACCAATGGGACCATGATGAGTATTTGATGGCATTTGCCAAATATAC 60
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QY 1018 ATGTTGCAATGCAAAATTTTGGAAAAATGACCTGCGCATGCAAAAACTATTAAT 1077
Db 781 ATGTTGCAATGCAATGCTGTTTGGAAAAATGACCTGCGCATGCAAAAACTATTAAT 840
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Db 841 AAAACAAGTTGGAATCACTCCGTTGCAATGTTCTCTCTTCAATTAATTTGTAACAATGCA 900
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QY 1198 CACCCTATACATGACGTCACATTTGTTGATTAACCATGACTCTGAGCCAGAGAGACATTG 1257
Db 961 CATCCACACATGCGCTTACTTTTGTGATTAACCATGATTTCTAGCCCGGAGAGCATTTG 1020
QY 1258 GAATCCTTTGTTCAATGCGTTTCAAAACCTGAGCATATGATTTGTTGACAAAGGAG 1317
Db 1021 GAATCCTTTGTTCAACATGATTTTAAACCACTTGACATGATGCTTGTTCGACAAAGGAA 1080

QY 1318 CAAGTTACCTTCGATTTTAAAGGTATTAACGGTATACCAACTCATGGTTCT 1377
 Db 1081 CAAGTTATCTTCGATTTTAAAGGTATTAACGGTATTAACCAACTCATGGTTCT 1140
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 Db 1141 GCTATGAATCTAAATGATGACCTTCGACGACCTCAACCTATGCTATGATG 1200
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 Db 1201 CAGATGATTTTATGATCATGATATTTATCGGCTGACGACGAGGAGCACTCC 1260
 QY 1498 CACCAATTCGACCTTCGACCTATTTATGCTGACGAGGAGGAGGAGGAGGAGG 1557
 Db 1261 CATCAATTCGACCTTCGACCTATTTATGCTGACGAGGAGGAGGAGGAGGAGG 1320
 QY 1558 TATGTCGGAACATTAAGCTGCGCAAGTATGAGAGATATCACCGAAATAGTCTGT 1617
 Db 1321 TATGTCGGAACATTAAGCTGCGCAAGTATGAGAGATATTAACCGAAATAGCAGGC 1380
 QY 1618 ACCGTACCATTAATGAGATGTTGGGGAATTTCACTGTAACGAGGAGGAGTTTCG 1677
 Db 1381 ACCGTACCATTAATGAGATGTTGGGGAATTTCTCTGTTAATGAGAGGAGGTTTCG 1440
 QY 1678 GTTGGGTGAAGCA 1692
 Db 1441 GTTGGGTGAAGCA 1455

RESULT 15

US-09-354-191A-4
 Sequence 4, Application US/09354191A
 Patent No. 6297038

GENERAL INFORMATION:
 APPLICANT: Bisgaard-Frantzen, Henrik
 APPLICANT: Svendsen, Allan
 APPLICANT: Borchert, Torben Vedel
 TITLE OF INVENTION: AMYLASE VARIANTS
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESS:
 ADDRESS: No. 62970380 No. 6297038disk of No. 6297038th America, Inc.
 STREET: 405 Lexington Avenue, Suite 6400
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10174-6401
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/354,191A
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/600,656
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Lambiris, Elias J.
 REGISTRATION NUMBER: 33,728
 REFERENCE/DOCKET NUMBER: 4318-204-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 867 0123
 TELEFAX: 212 867 0298
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1455 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)

US-09-354-191A-4

Query Match 65.74; Score 1167; DB 3; Length 1455;
 Best Local Similarity 87.68; Pred. No. 0;
 Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

QY 238 CATCATATGAGGAGGAATGGGACCATGATGATGATTTTGAATGGGATTTGCCAATATAC 297
 Db 1 CATCATATGAGGAGGAATGGGACCATGATGATGATTTTGAATGGGATTTGCCAATATAC 60
 QY 298 GGGAAACCACTGGAACAGGTTACGATGACGACCTAACCTTAAAGATTAAGGATTAAC 357
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GenCore version 5.1.6
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Searched: 5642217 seqs, 3043843248 residues 11284434
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1776	100.0	1786	9	US-09-971-611-1
4	1776	100.0	1786	18	US-10-798-278-1
5	1170	65.9	1458	16	US-10-184-771-11
6	1170	65.9	1458	19	US-10-926-720-11
7	1167	65.7	1455	9	US-09-768-864-9
8	1167	65.7	1455	9	US-09-768-864-13
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10	1167	65.7	1455	9	US-09-902-188A-4
11	1167	65.7	1455	9	US-09-918-543-1

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13	1167	65.7	1455	14	US-10-025-648-4	Sequence 4, Appli
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ALIGNMENTS

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Sequence 1, Application US/09986676A
Patent No. US20020102698A1
GENERAL INFORMATION:
APPLICANT: HATADA, Yuji
APPLICANT: OZAKI, Katsuya
APPLICANT: ARA, Katsutoshi
APPLICANT: KAWAI, Shuji
TITLE OF INVENTION: Gene Encoding Alkaline Liquefying Alpha-Amylase
FILE REFERENCE: 2173-0121P
CURRENT APPLICATION NUMBER: US/09/986, 676A
PRIOR FILING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: PCT/JP96/01641
PRIOR FILING DATE: 1996-06-14
PRIOR APPLICATION NUMBER: Japan 147257/1995
PRIOR FILING DATE: 1995-06-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1776
TYPE: DNA
ORGANISM: Bacillus sp.
FEATURE:
NAME/KEY: CDS
LOCATION: (145)..(1692)
OTHER INFORMATION:
US-09-986-676A-1
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1776; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Publication No. US20040091994A1
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; APPLICANT: Andersen, Carsten
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; FILE REFERENCE: 10115.204-WO
; CURRENT APPLICATION NUMBER: US/10/399,161
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
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; LOCATION: (145)..(238)
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; LOCATION: (238)..()

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APPLICANT: ARAKI, HIROYUKI
 APPLICANT: ENDO, KEIJI
 APPLICANT: HAGIHARA, HIROSHI
 APPLICANT: IGARASHI, KAZUAKI
 APPLICANT: HAYASHI, YASUHIRO
 APPLICANT: OZAKI, KATSUYA
 TITLE OF INVENTION: HIGHLY PRODUCTIVE ALPHA-AMYLASES
 FILE REFERENCE: 214377USO
 CURRENT APPLICATION NUMBER: US/10/798,278
 PRIOR FILING DATE: 2004-03-12
 PRIOR APPLICATION NUMBER: US/09/971,611
 PRIOR FILING DATE: 2001-10-09
 PRIOR APPLICATION NUMBER: JP 2000/310605
 PRIOR FILING DATE: 2001-10-11
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 DB 1271 TCCCTTTGCAATGCTGTTCAACCACTGGCAATGATTTGTAACAAAGGAGCA 1330
 QY 1321 GGTACCCCTTCGATATTTTACGATATTAATCAAGGTAATCAATGATGTTCTTTCG 1380
 DB 1331 GGTACCCCTTCGATATTTTACGATATTAATCAAGGTAATCAATGATGTTCTTTCG 1390
 QY 1381 ATGAATCTTAATATGATCACTTCTGCAAGCAGTCAAAAGTATGCTTACGGAACCAA 1440
 DB 1391 ATGAATCTTAATATGATCACTTCTGCAAGCAGTCAAAAGTATGCTTACGGAACCAA 1450
 QY 1441 CATGATTTTGTGATCATGATATTTATGCGCTGAGCAGAGAAAGGGAACAGCTCCAC 1500
 DB 1451 CATGATTTTGTGATCATGATATTTATGCGCTGAGCAGAGAAAGGGAACAGCTCCAC 1510
 QY 1501 CCAATTTCAAGGACTTGCAACATTAATGTCGATGAGGCAAGGAGGTAATTAATGATGAT 1560
 DB 1511 CCAATTTCAAGGACTTGCAACATTAATGTCGATGAGGCAAGGAGGTAATTAATGATGAT 1570
 QY 1561 GTGCGGAAACATTAAGCTGCGCAAGTATGAGAGATATCACCGGAAATAGGTCTGTACC 1620
 DB 1571 GTGCGGAAACATTAAGCTGCGCAAGTATGAGAGATATCACCGGAAATAGGTCTGTACC 1630

Db	301	GGTGAATGTCGATCAGATCATTAAGGTGGAGACATGGTACCGAAATTGTAAATGCGGTA	360
Qy	598	GAAGTGAACCGAGCAACCGAAACCAAGAAATATCAGGTAAATACACATTGAAGCATGG	657
Db	361	GAAGTGAATGGAGCAACCGAAACCAAGAAACCTCAGAGAGTATGCAATGGAAGCGTGG	420
Qy	658	ACGAAATTTGATTTCCCTGGAAAGGAAATACCATTTCAACTTTAAATGGCGCTGGTAT	717
Db	421	ACAAAGTTTGATTTTCTTGAAAGGAAATBACATTTCCAGCTTTTAAGTGGCGCTGGTAT	480
Qy	718	CATTGTGATGGGACAGATTGGGATCAGTCACTGACGCTTCAGAACAAATATATTAATTC	777
Db	481	CATTGTATGGGACAGATTGGGATCAGTCACTGACGCGAGCTTCAAACAAATATATTAATTC	540
Qy	778	AGAGTACCCGAAAGGCAATGGGACTGGGAAAGTATATATAGAAACGGCACTATGATTAC	837
Db	541	AGGGGAACAAGGCAAGCGCTGGGACTGGGAAAGTCAATAGAGAAATGCAACTATGACTAT	600
Qy	838	CTTATGTATCGAGCATTTGATATAGATCATCCAAAGTAATCANTGAACCTTAGAAATTGG	897
Db	601	CTTATGTATCGAGCGTGGATATGATATCACCBAAGTAATATGAATTTAGAAACTGG	660
Qy	898	GGAGTTTGATATCAAAATACACTTAATCTAGATGATTTAGAAATCGATGCTGTGAACAT	957
Db	661	GGAGTGTGTRATGGAATACACTGACACTTGATGATTTAGAAATAGATGCAGTGAACAT	720
Qy	958	ATTAAATACAGACTATACGAGAGATTGGCTAACACATGTGCGTAAACACACAGTAAACA	1017
Db	721	ATAAATATATAGCTTTACGAGAGATTGGCTTAACATGTGCGTAAACACACAGTAAACA	780
Qy	1018	ATGTTTGACGTGGAGAAATTTTGGAAAAAGACCTTGCTGCAATCGAAACATATTTAAT	1077
Db	781	ATGTTTGACAGTGGAGTTTGGAAAAAGACCTTGCTGCAATTTGAAACATATTTGAT	840
Qy	1078	AAAACAAGTTGGAATCACTCGGTGTGGATGTTCTCTTCATTAATTTGTACAAATGCA	1137
Db	841	AAAACAAGTTGGAATCACTCGGTGTGGATGTTCTCTTCATTAATTTGTACAAATGCA	900
Qy	1138	TCTAATAGTGGTACTATTTTGATATGAGAAATTTTAAATGGTCTGTGTCACAAA	1197
Db	901	TCTAATAGCGGTGTTATTTATGATATAGAAATTTTAAATGGTCTGTGTCACAAA	960
Qy	1198	CACCTTATPACATGCACTCATTTGTTGATPACATGACTTCAGGCCAGGAAAGCATTG	125
Db	961	CATCAACAACATGCGCTTACTTTGTTGATPACATATTCCTCAGCCCGGGAAGCATTG	1020
Qy	1258	GAATCCCTTTGTCAAATGTTGGTTCAAAACACTGGCATATGATGATTCTGACAAAGGAG	1317
Db	1021	GAATCCCTTTGTCAAATGTTGTTAAACCACTGGCATATGATTGTTCTGACAAAGGAA	108
Qy	1318	CAAGTTTACCTTCOGATTTTTCAGTGATTTACTACGGTATACCACTCATGTTGTTCT	1377
Db	1081	CAAGTTTATCTTCOGATTTTTCAGTGATTTACTACGGTATCCCAACCATGTTGTTCTG	1144
Qy	1378	TCGATGAATCTAAATTTGATCACTTCTGCAAGCAAGTCAAAGTATGCTTAGCGAAAC	1437
Db	1141	GCTATGAAATCTAAATTTGACCCCTCTTCTGCAAGCAAGTCAAACCTTTTGCTTATGTA	1200
Qy	1438	CAATATATTTATTTGATCATCATGATATTAATGGGCTGGAGAGAGAAAGGGGACAGCTCC	1497
Db	1201	CAGATATATTTATTTGATCATCATGATATTAATGGGCTGGAGAGAGAGAAATATGCTCC	1266
Qy	1498	CACCAAAATTCAGGACTTGCACATTAATATGTCAGATGGGCCAGGGGGTAAATTAATGATG	155
Db	1261	CATCAAAATTCAGGACTTGCACCATATATATGTCAGATGGTCCAGGTGGTAAACAAATGATG	1322
Qy	1558	TATGTGGGAAACATAAAGCTGGCCAGATATGAGAGATATCACCGGAATATAGTCTGGT	1617
Db	1321	TATGTGGGAAATTAAGCGGGACAAGTTTGGAGATATTTAACCGGAATATGACAAGGC	1380
Qy	1618	ACCTTCACATTAATGACAGATGTTGGGGGAATTTCACTGTAACCGGAGGGGCAAGTTTCG	1677

Db 1381 ACCGTCACAAATTAATGACAGCGATGGGTAATTTCTCTGTAAATGAGGGTCGTTTCG 1440
Qy 1678 GTTGGGTGAAGCAATA 1695
Db 1441 GTTGGGTGAAGCAATA 1458

RESULT 7

US-09-769-864-9
; Sequence 9, Application US/09769864
; Patent No. US20010039253A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nielsen, Torben L.
; APPLICANT: Kjaerulf, Soren
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/769,864
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/183,412
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Bacillus
; US-09-769-864-9

Query Match 65.7%; Score 1167; DB 9; Length 1455;

Best Local Similarity 87.6%; Pred. No. 4e-302;

Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

Qy 238 CATCATTAATGGAGGAATGGACCATGATGACGATTTTGAATGGCAATTTGCCAAATGAC 297
Db 1 CATCATTAATGGAGGAATGGACCATGATGACGATTTTGAATGGCAATTTGCCAAATGAC 60
Qy 298 GGGAAACACTGGAAACAGGTTCAGAGATGACGACGCTTAATTAAGATTAAGGATTAAC 357
Db 61 GGGAAATCATTTGGAACAGGTTCAGAGATGACGACGCTTAATTAAGATTAAGGATTAAC 120
Qy 358 GCTGTTGATTCCTCTGATGAGGAGGAGCTTCGCAAAATGATGTTGGATGAGCC 417
Db 121 GCTGATGATTCCTCACTGATGAGGAGGAGCTTCGCAAAATGATGTTGGATGAGCC 180
Qy 418 TATGATTTGATGATCTTGGTGAATTAACCAAAAGGAAACGTCGTAACAAATATGAC 477
Db 181 TATGATTTATATATCTTGGAGATTTAACCAAAAGGAGGACGTCGTAACAAATATGAC 240
Qy 478 ACAAGAGTGAATGCAAGGTGCGGAGCATCTTTGAAAATAACGGGATTCAGATTTAT 537
Db 241 ACAAGAGTGAATGCAAGGTGCGGAGCATCTTTGAAAATAACGGGATTCAGATTTAT 300
Qy 538 GGGGATGCTGATGATCATTAAGGTGAGACAGCGACAGAGATGTAATGCGGTG 597
Db 301 GGTGATGCTGATGATCATTAAGGTGAGACAGATGTAATGTAATGCGGTG 360
Qy 598 GAAGTGAACCGAAGCAACCGAAGCAAAATATCAGTGAATACCAATTAAGCATGG 657
Db 361 GAAGTGAATCGAGCAACCGAAGCAAAATCAGGAGATGATGCAATTAAGCATGG 420
Qy 658 ACGAATTTATTTCTCTGGAAGAGAAATACCATTTCCAACTTTAATGGCGCTGTAT 717
Db 421 ACGAATTTATTTCTCTGGAAGAGAAATACCATTTCCAACTTTAATGGCGCTGTAT 480
Qy 718 CATTTGATGGGACAGATGGGATCACTGACGCTGAGCTTACAGCAAAATATTAATTC 777
Db 481 CATTTGATGGGACAGATGGGATCACTGACGCTGAGCTTACAGCAAAATATTAATTC 540
Qy 778 AGAGGTACCGAAGAGCATGGAGCTGGGAATGATATAGAGAACGCAACTATGATTAAC 837

Db 541 AGGGAACAGGAGGCGCTGGGACTGGGAAGTGCATACAGAGATGGCAACTATGACTAT 600
Qy 838 CTATATGATGACAGACTTGTATATGATCATCCAGAGATTAATCAATTAATTAATTCG 897
Db 601 CTATATGATGACAGACTTGTATATGATCATCCAGAGATTAATCAATTAATTAATTCG 660
Qy 898 GGAGTTGGTATCAATATCACTTAATCTGATGATTAATGATCGATGCTGAATCAT 957
Db 661 GGAGTTGGTATCAATATCACTTAATCTGATGATTAATGATCGATGCTGAATCAT 720
Qy 958 ATTAAATACAGCTATACAGAGATGGCTTAACATGTCGTACACCAAGGTAACCA 1017
Db 721 ATTAAATACAGCTATACAGAGATGGCTTAACATGTCGTACACCAAGGTAACCA 780
Qy 1018 ATGTTGAGTTCAGAAATTTGGAAAATATGACCTTGGCAATGCAAACTATTAAT 1077
Db 781 ATGTTGAGTTCAGAAATTTGGAAAATATGACCTTGGCAATGCAAACTATTAAT 840
Qy 1078 AAAACAGTTGGATCACTCCGTTGATGATGATGATGATGATGATGATGATGATGAT 1137
Db 841 AAAACAGTTGGATCACTCCGTTGATGATGATGATGATGATGATGATGATGATGAT 900
Qy 1138 TCTAATAGTGGTGGTATTTGATGATGATGATGATGATGATGATGATGATGAT 1197
Db 901 TCTAATAGTGGTGGTATTTGATGATGATGATGATGATGATGATGATGATGAT 960
Qy 1198 CACCCATACAGGACATCACTTGTGATTAACCAATGATGATGATGATGATGATGAT 1257
Db 961 CACCCATACAGGACATCACTTGTGATTAACCAATGATGATGATGATGATGATGAT 1020
Qy 1258 GAATCCTTTGTCATCGTGTTCATCAACACATGACATGATGATGATGATGATGATGAT 1317
Db 1021 GAATCCTTTGTCATCGTGTTCATCAACACATGATGATGATGATGATGATGATGAT 1080
Qy 1318 CAAGTTACCTTCGATTTTACGATGATTAACGATGATTAACCAATGATGATGAT 1377
Db 1081 CAAGTTACCTTCGATTTTACGATGATTAACGATGATTAACCAATGATGATGAT 1140
Qy 1378 TCGATTAATCTTAATTAATGATCACTTCGAGGAGCGCAACGATGATGATGATGAT 1437
Db 1141 GCTATTAATCTTAATTAATGATCACTTCGAGGAGCGCAACGATGATGATGATGAT 1200
Qy 1438 CAACATGATTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1497
Db 1201 CAGCATGATTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
Qy 1498 CACCCAAATTCAGGATTCGAACTATTAATGATGATGATGATGATGATGATGATGAT 1557
Db 1261 CACCCAAATTCAGGATTCGAACTATTAATGATGATGATGATGATGATGATGATGAT 1320
Qy 1558 TATGTCGGGAAACATTAAGCTGGCCCAAGATGAGATGATGATGATGATGATGAT 1617
Db 1321 TATGTCGGGAAACATTAAGCTGGCCCAAGATGAGATGATGATGATGATGATGAT 1380
Qy 1618 ACCGTCACCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1677
Db 1381 ACCGTCACCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
Qy 1678 GTTGGGTGAAGCA 1692
Db 1441 GTTGGGTGAAGCA 1455

RESULT 8

US-09-769-864-13
; Sequence 13, Application US/09769864
; Patent No. US20010039253A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne

Query Match 65.7%; Score 1167; DB 9; Length 1455;
 Best Local Similarity 87.6%; Pred. No. 4e-302; Indels 0; Gaps 0;
 Matches 1275; Conservative 0; Mismatches 180;

QY 238 CATCATATGGAAGCAATGGGACCATGATGAGTATTTGATGAGCATTTGCCAAATGAC 297
 Db 1 CATCATATGGAAGCAATGGGACCATGATGAGTATTTGATGAGCATTTGCCAAATGAC 60

QY 298 GGGAAACCATGGAACAGGTTACGAGATGACGACGCTAATTAAAGATTAAGGATTAAC 357
 Db 61 GGGAAATCATGGAACAGGTTAGAGGATGACGACGCTAATTAAAGATTAAGGATTAAC 120

QY 358 GCGTTGATGATCTCTCGATGGAAGGAGCTGCAAAATGATGTTGGGTATGGGCC 417
 Db 121 GCGTATGATGATCCACCTGATGGAAGGAGCTTCCAAATGATGTTAGTATGAGGCC 180

QY 418 TATGATTTGATGATCTTGTGATGATTTACCAAAAGGAAACGTCCTACAAATATGAC 477
 Db 181 TATGATTTATATGATCTTGGAGATTTACCAAGAGGAGCGGTTGCTACAAATATGGA 240

QY 478 ACAAGAGTCAATGTCAGAGTCCGCTGACATCTTTGAAAAATACGGGATTTCAAGTTAT 537
 Db 241 ACAAGCAACAGGATCAAGGCTGCGGTGACCTTTTAAAAATACCGCATTCAGTATAT 300

QY 538 GGGGATGTCGATGATCAATCAATTAAGTGAAGACAGGACAGAGATGTTAAATGCGGTG 597
 Db 301 GGTGATGTCGTCATGATCAATTAAGTGAAGACAGTGTACGAAATTTGAAATGCGGTG 360

QY 598 GAAATGACCGAAGCAACCGAAACCAAAATATCAGTGAATACCATTTGAAGCATGG 657
 Db 361 GAAATGATCGAGCAACCGAAACCAAAATATCAGGATGATGCAATTAAGACGTTGG 420

QY 658 ACCGAATTTGATTTCCCTGGAAGGAAATACCATTTCCAACTTTAAATGGCGTGTAT 717
 Db 421 ACAAGATTTATTTTCTTGGAAGGAAATACCATTTCCAGCTTTAAAGTGGCGTGTAT 480

QY 718 CATTTGATGGAAGATGGAATCATGATCACTGATGATGATGATGATGATGATGATGAT 777
 Db 481 CATTTGATGGAAGATGGAATCATGATCACTGATGATGATGATGATGATGATGATGAT 540

QY 778 AGAGGTACCGGAAAGGATGGAATGGAATGATGATGATGATGATGATGATGATGAT 837
 Db 541 AGGGGAACAGGCAAGGCTGGGATCTGGGAAGTCAATACAGAGATGCACTATGAT 600

QY 838 CTTATGATGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 897
 Db 601 CTTATGATGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660

QY 898 GGAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 957
 Db 661 GGAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720

QY 958 ATTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1017
 Db 721 ATTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780

QY 1018 ATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1077
 Db 781 ATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840

QY 1078 AAAACAAGTGAATCACTCCGTTGATGATGATGATGATGATGATGATGATGAT 1137
 Db 841 AAAACAAGTGAATCACTCCGTTGATGATGATGATGATGATGATGATGATGAT 900

QY 1138 TCTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1197
 Db 901 TCTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960

QY 1198 CACCTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1257
 Db 961 CACCTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020

QY 1258 GAATCTTTGTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1317

Db 1021 GATCTTTGTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080

QY 1318 CAAGTTACCTTCGATATTTTACGATGATGATGATGATGATGATGATGATGAT 1377

Db 1081 CAAGTTATCTTCCTATTTTATGAGGATGATGATGATGATGATGATGATGATGAT 1140

QY 1378 TCGATGAATCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1437

Db 1141 GCTATGAATCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200

QY 1438 CAACATGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1497

Db 1201 CAGCATGATTTATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260

QY 1498 CACCAATTCAGGATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1557

Db 1261 CACCAATTCAGGATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320

QY 1558 TATGTCGGAACATTAAGCTGCGCAAGTATGAGAGATATCACCGAAATAGTCTGAT 1617

Db 1321 TATGTCGGAACATTAAGCTGCGCAAGTATGAGAGATATTAACCGAAATAGGACAGG 1380

QY 1618 ACCGTACCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1677

Db 1381 ACCGTACCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440

QY 1678 GTTTGGGTGAAGCA 1692

Db 1441 GTTTGGGTGAAGCA 1455

RESULT 10

US-09-902-188A-4

Sequence 4, Application US/09902188A

Patent No. US2002009896A1

GENERAL INFORMATION:

APPLICANT: Bisgard-Frantzen, Henrik

Svendsen, Allan

Borchert, Torben Vedel

TITLE OF INVENTION: AMYLASE VARIANTS

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSER: No. US2002009896A10 No. US2002009896A1disk of No. US2002009896;

STREET: 405 Lexington Avenue, Suite 6400

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10174-6401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/902,188A

FILING DATE: 10-Jul-2001

CLASSIFICATION: <Unknown>

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 09/354,191

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Lambiris, Elias J.

REGISTRATION NUMBER: 33,728

REFERENCE/DOCKET NUMBER: 4318, 204-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212 867 0123

TELEFAX: 212 867 0298

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 1455 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-902-188A-4

Query Match 65.7%; Score 1167; DB 9; Length 1455;
Best Local Similarity 87.6%; Pred. No. 4e-302;
Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

238 CATCATATATGGAGAGATGGAGACCATGATGCAATTTTGAATGGCATTTGCCAAATAC 297
1 CATCATATATGGAGAGATGGAGACCATGATGCAATTTTGAATGGCATTTGCCAAATAC 60
298 GGAACCACTGGAACAGGTTACGAGATGACGAGCTAATTAAGATGAAGGATTAAC 357
61 GGAATCATTTGGAACAGGTTACGAGATGACGAGCTAATTAAGATGAAGGATTAAC 120
358 GCTGTTGGATTCCTCTGATGAGAGGGAATTGCAAAATGATGTTGGTATGTC 417
121 GCTGATGAGATCCACCTGATGAGAGGGAATTGCAAAATGATGTTATGAGACC 180
418 TATGATTTGATGATCTTGTGATTTAACCAAAAGGAAACCGTCCGTAATAATATG 477
181 TATGATTTGATGATCTTGTGATTTAACCAAAAGGAAACCGTCCGTAATAATATG 240
478 ACAAGAGTCACTGGAAGGAGTGCCTGATCTTTGAATAACGGGATCAAGTTAT 537
241 ACAGCAGACAGCTACAGGCTGCGGTGCTTTTAAATAAATACGGGATCAAGTTAT 300
538 GGGGATGCTGATGATCATTAAGTGGAGACAGGAGACAGATGATTAATGCGGTG 597
301 GGTGATGCTGATGATCATTAAGTGGAGACAGGAGACAGATGATTAATGCGGTG 360
598 GAAATGACCAAGACCAAGAAACCAAGAAATATCAGGTGAATACCATTTGAAGCAT 657
361 GAAATGACCAAGACCAAGAAACCAAGAAATATCAGGTGAATACCATTTGAAGCAT 420
658 ACGAAATTTGATTTCCCTGGAAGAGAAATACCATTTCAACTTTAATGGCGGTAT 717
421 ACGAAATTTGATTTCCCTGGAAGAGAAATACCATTTCAACTTTAATGGCGGTAT 480
718 CATTTGATGAGACAGATTTGGGATCAGTCAGTCAGTTCCAGAACAAATATATATTC 777
481 CATTTGATGAGACAGATTTGGGATCAGTCAGTCAGTTCCAGAACAAATATATATTC 540
778 AGAGATACCGGAAAGCATGAGGAGTGGAGATGATATAGAAACGAGCACTATGATTAC 837
541 AGGGAACAGGCAAGGCTGGGAGCTGGGAGATGATATAGAAACGAGCACTATGATTAC 600
838 CTATATGATGAGACATTTGATGATGATATCCAGAAATGATATGAACTTGAATTTG 897
601 CTATATGATGAGACATTTGATGATGATATCCAGAAATGATATGAACTTGAATTTG 660
898 GGAGTTGGTATTAACAAATACCTTAATAGATGATTTGAATGATGATGATGATGAT 957
661 GGAGTTGGTATTAACAAATACCTTAATAGATGATTTGAATGATGATGATGATGAT 720
958 ATTAAATACAGCTATACAGAGATTTGGCTAACATGTCGTAACACCAAGTAAACCA 1017
721 ATAAATATACCTTTAGAGAGATTTGGCTTAACATGTCGTAACACCAAGTAAACCA 780
1018 ATGTTTGCAGTTGCAAGATTTTGGAAAAATGACCTGCTGCAATGAAAACTATTTAAT 1077
781 ATGTTTGCAGTTGCAAGATTTTGGAAAAATGACCTGCTGCAATGAAAACTATTTAAT 840
1078 AAAACAAGTTGGAATCACTCCGTTGATGATGATGATGATGATGATGATGATGAT 1137
841 AAAACAAGTTGGAATCACTCCGTTGATGATGATGATGATGATGATGATGATGAT 900
1138 TCTAATAGTGTGCTATTTTGAATGAGAAATATTTAAATGTTCTGTCGTAACAAA 1197
901 TCTAATAGTGTGCTATTTTGAATGAGAAATATTTAAATGTTCTGTCGTAACAAA 960

1198 CACCTATATACATGAGTACATTTGTTGATTAACATGATCTCTACGACGAGAGATG 1257
961 CATCAACATATGCGGTACTTTGTTGATTAACATGATCTCTACGACGAGAGATG 1020
1258 GAATCTTTGTTCAATCTGTTGTTCAACCATCTGCGATATGATTTGTTGCAAGGAG 1317
1021 GAATCTTTGTTCAATCTGTTGTTCAACCATCTGCGATATGATTTGTTGCAAGGAG 1080
1318 CAAGTTACCTTCGATTTTGAATGATGATGATGATGATGATGATGATGATGATGAT 1377
1081 CAAGTTACCTTCGATTTTGAATGATGATGATGATGATGATGATGATGATGATGAT 1140
1378 TCGATGAATCTAAATTTGATGATGATGATGATGATGATGATGATGATGATGAT 1437
1141 GCTATGAATCTAAATTTGATGATGATGATGATGATGATGATGATGATGATGAT 1200
1438 CAACATGATTTATTTGATGATGATGATGATGATGATGATGATGATGATGAT 1497
1201 CAGCATGATTTACTTTGATGATGATGATGATGATGATGATGATGATGATGAT 1260
1498 CACCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1557
1261 CATCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
1558 TATGCGGAAACATTAAGTGGGCAAGTATGAGAGATATCAACGAAATAGTCTG 1617
1321 TATGCGGAAACATTAAGTGGGCAAGTATGAGAGATATCAACGAAATAGTCTG 1380
1618 ACCGTCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1677
1381 ACCGTCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
1678 GTTGGGTGAAGCA 1692
1441 GTTGGGTGAAGCA 1455

RESULT 11

US-09-918-543-1
Sequence 1, Application US/09918543
Patent No. US20020155574A1
GENERAL INFORMATION:
APPLICANT: No. US20020155574A1ozymes A/S
APPLICANT: Thisted, Thomas
APPLICANT: Kjaerulf, Soren
APPLICANT: Andersen, Carsten
APPLICANT: Fuglsang, Claus Crone
TITLE OF INVENTION: Alpha-amylase mutants with altered properties
FILE REFERENCE: 10062.200-US
CURRENT APPLICATION NUMBER: US/09/918,543
CURRENT FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1455
TYPE: DNA
ORGANISM: Bacillus sp.
FEATURE:
NAME/KEY: CDS
LOCATION: (1) ..(1455)
OTHER INFORMATION:
US-09-918-543-1

Query Match 65.7%; Score 1167; DB 9; Length 1455;
Best Local Similarity 87.6%; Pred. No. 4e-302;
Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

238 CATCATATATGGAGAGATGGAGACCATGATGCAATTTTGAATGGCATTTGCCAAATAC 297
1 CATCATATATGGAGAGATGGAGACCATGATGCAATTTTGAATGGCATTTGCCAAATAC 60
298 GGAACCACTGGAACAGGTTACGAGATGACGAGCTAATTAAGATGAAGGATTAAC 357

```
Db 61 GGGAAATCATTGGAACAGGTTGAGGATGACGAGCTAACTTAAGAATAAGGGATATA 120
QY 358 GCTGTTGGATTCCTCTGATGGAAGGGAATTCGCAAAATGATGTTGGGTATGCTGCC 417
Db 121 GCTGATGATGCCACCTGATGGAAGGGGACTTCCAGATATGATGATGATGAGGCC 180
QY 418 TATGATTTGATGAGCTGTTGATGATTAACCAAAAGGGAACCGTCCGTACAAATATGCG 477
Db 181 TATGATTTATATATCTTGAGAGTTTACCAAGAGGGGACGGTGTGTCATAAATATGGA 240
QY 478 ACAAGAGTCAGTTGCAAGGTGCGTGAATCTTGTGAAAAATAACGGATTCAGTTTAT 537
Db 241 ACACGACACAGCTTACAGGCTGCGGTGACCTCTTAAAAATAACGGCATTCAGTATAT 300
QY 538 GGGGATGTCGTGATGATCATTAAGGTGACGACGAGCAAGATGATGTAATGCGGTG 597
Db 301 GGTGATGTCGTATGATCATTAAGGTGAGCAGATGTTACGGAATTTGTAATGCGGTG 360
QY 598 GAAGTGAACCGGAACACGGAACCAAGAAATATCAGTGAATACCAATGGAAGCATGG 657
Db 361 GAAGTGAATGAGCAACCGAAACCAAGAAACCTCAGAGAGATGATGATGAGAGCGTGG 420
QY 658 ACAGAAATTTGATTCCTCTGGAAGAGAAATATCCCATTTCAACTTTAATGCGCTGTAT 717
Db 421 ACAGATTTGATTTCTCTGGAAGAGAAATATACCATTTCCAGCTTTAAGTGGCGTGTAT 480
QY 718 CATTTGATGGGACAGATTTGGGATCAGTCACTGATGCTTGAACAAATATATTAATTC 777
Db 481 CATTTGATGGGACAGATTTGGGATCAGTCACTGATGCTTGAACAAATATATTAATTC 540
QY 778 AGAGTGAACCGGAAGGATGGAAGTGAAGTATGAGAGACGGAACCTATGATTTAC 837
Db 541 AGGGGAACAGGACAGGCTGAGGACTGGAGATGATGATGATGATGATGATGATGAT 600
QY 838 CTATGATGACAGCATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 897
Db 601 CTATGATGACAGCATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 898 GGAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 957
Db 661 GGAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
QY 958 ATTAATATACAGTATACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1017
Db 721 ATTAATATACAGTATACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
QY 1018 ATGTTTGCAGTTGACAGATTTTGAAGAAATGACCTTGTCTGCAATGCAATTAAT 1077
Db 781 ATGTTTGCAGTTGACAGATTTTGAAGAAATGACCTTGTCTGCAATGCAATTAAT 840
QY 1078 AAAACAAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1137
Db 841 AAAACAAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
QY 1138 TCAATATAGTGGGCTATTTTGAATGAGAAATATTTAATGATGATGATGATGATGAT 1197
Db 901 TCAATATAGTGGGCTATTTTGAATGAGAAATATTTAATGATGATGATGATGATGAT 960
QY 1198 CACCTATACATGACAGTCAATTTGTTGATGATGATGATGATGATGATGATGATGAT 1257
Db 961 CACCTATACATGACAGTCAATTTGTTGATGATGATGATGATGATGATGATGATGAT 1020
QY 1258 GAATCTTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1317
Db 1021 GAATCTTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
QY 1318 CAAGTTTACCTTCCGATTTTACGAGTATGATGATGATGATGATGATGATGATGATGAT 1377
Db 1081 CAAGTTTATCTTCCGATTTTATGAGGATATGATGATGATGATGATGATGATGATGAT 1140
QY 1378 TCGATGAATCTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1437
Db 1141 GGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
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QY 1438 CAACATGATTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1497
Db 1201 CAGCATGATTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
QY 1498 CACCAATATTCAGACCTTGCACATATATGATGATGATGATGATGATGATGATGATGAT 1557
Db 1261 CATTCAATTTGAGGCTTGCACATATATGATGATGATGATGATGATGATGATGATGAT 1320
QY 1558 TATGTCGGGAACATTAAGCTGCGCAGATGATGATGATGATGATGATGATGATGATGAT 1617
Db 1321 TATGTCGGGAACATTAAGCTGCGCAGATGATGATGATGATGATGATGATGATGATGAT 1380
QY 1618 ACCGTACCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1677
Db 1381 ACCGTACCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
QY 1678 GTTGGGTGAAGCAA 1692
Db 1441 GTTGGGTGAAGCAA 1455

RESULT 12
US-09-925-576C-1
; Sequence 1, Application US/0925576C
; Publication No. US20030129718A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; APPLICANT: Borcherdt, Torben Vedel
; APPLICANT: Nielsen, Bjarne Ronfeldt
; TITLE OF INVENTION: Amylase Variants
; FILE REFERENCE: 10004.204-US
; CURRENT APPLICATION NUMBER: US/09/925,576C
; NUMBER OF SEQ ID NOS: 20
; FILING DATE: 2001-08-09
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Bacillus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1455)
; OTHER INFORMATION: SP690
US-09-925-576C-1

Query Match 65.7%; Score 1167; DB 10; Length 1455;
Best Local Similarity 87.6%; Pred. No. 4e-302;
Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

QY 238 CATCATATATGGAACGAATGGGACCATGATGATGATGATGATGATGATGATGATGATGAT 297
Db 1 CATCATATATGGAACGAATGGGACCATGATGATGATGATGATGATGATGATGATGATGATGAT 60
QY 298 GGGAACTATGGAACAGTTTACAGATGACGACGATTAACCTTAAGAGTAAAGGATTAAC 357
Db 61 GGGAACTATGGAACAGTTTACAGATGACGACGATTAACCTTAAGAGTAAAGGATTAAC 120
QY 61 GGGAACTATGGAACAGTTTACAGATGACGACGATTAACCTTAAGAGTAAAGGATTAAC 120
Db 61 GGGAACTATGGAACAGTTTACAGATGACGACGATTAACCTTAAGAGTAAAGGATTAAC 120
QY 358 GCTGTTGATTCCTCTGATGGAAGGGAAGGGAAGGGAAGGGAAGGGAAGGGAAGGGAAG 417
Db 121 GCTGTTGATTCCTCTGATGGAAGGGAAGGGAAGGGAAGGGAAGGGAAGGGAAGGGAAG 180
QY 418 TATGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 477
Db 181 TATGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
QY 478 ACAAGAGTCAGTTGCAAGGTGCGTGAATCTTGTGAAAAATAACGGATTCAGTTTAT 537
Db 241 ACACGACACAGCTTACAGGCTGCGGTGACCTCTTAAAAATAACGGCATTCAGTATAT 300
QY 538 GGGGATGTCGTGATGATCATTAAGGTGACGACGAGCAAGATGATGTAATGCGGTG 597
Db 301 GGTGATGTCGTATGATCATTAAGGTGAGCAGATGTTACGGAATTTGTAATGCGGTG 360
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OY	538	GAAGTGAACCGAAGAACCGAATACCAAGAAATATACAGGTATDACAACCTTGAAGATGG	657
Db	361	GAAGTGAATCGAGACACCGAATCCAGAAACCTCAGAGAGATATGCAATTAAGACGTGG	420
OY	658	ACGAATTTGATTTCCCTGGAGAGAAATATCCCATTTCCAACTTTAAATGCGCTGTAT	717
Db	421	ACAAAGTTGATTTTCTGTGAAGAGAAATTAACATTCAGCTTTAAGTGGCGCTGTAT	480
OY	718	CATTTTGAATGGACGATTTGGGATCAGTCAGCTCAGCTTCAGAACAAATATATAATTC	777
Db	481	CATTTTGAATGGACGATTTGGGATCAGTCAGCTCAGCTTCAAACCAAAATATATAATTC	540
OY	778	AGAGGTACCGGAAAGCATTGGGACCTGGGAAGTATATAGAAACCGCAACTATATTC	837
Db	541	AGGGAAACGGCAAGGACCTGGGACCTGGGAAGTCGATACAGAAATGGCAACTATATAT	600
OY	838	CTTATGTATGCAGACATTGATATATGATCATCCAGAAATATCAATGAACCTTAGAAATGG	897
Db	601	CTTATGTATGCAGACGTGATATGATCATCCAGAAATATATCAATGAACCTTAGAAATGG	660
OY	898	GGAGTTGGTATACAAATACACTTAATCTAGATGGAATTTAGAATCGATGCTGTAAACAT	957
Db	661	GGAGTGGTATACAAATACACTTAATCTAGATGGAATTTAGAATCGATGCTGTAAACAT	720
OY	958	ATTAATATACAGTATACAGAGATTTGGCTTACACATGTGCGTAAACCAACAGATTAACCA	1011
Db	721	ATTAATATATAGCTTTTACAGAGATTTGGCTTACACATGTGCGTAAACCAACAGATTAACCA	780
OY	1018	ATGTTTGAAGTTGCAGAAATTTTGGAAAAATGACCTTGGCGCAATGGAAACATATTAAT	1077
Db	781	ATGTTTGAAGTTGCAGATTTTGGAAAAATGACCTTGGCGCAATGGAAACATATTTGAT	840
OY	1078	AAAACMAAGTTGGAATCACTCCGCTGTGCAATGTTCTCTTCATTATTAATTTTGAACATGA	1137
Db	841	AAAACMAAGTTGGAATCACTCCGCTGTGCAATGTTCTCTTCATTATTAATTTTGAACATGA	900
OY	1138	TCTAATAGTGGCTATTTTGGATATAGAAATATTTTAAATGTTCTGTGCTACAAAA	1197
Db	901	TCTAATACCGGTGTATTTATGATATAGAAATATTTTAAATGTTCTGTGCTGCAAAAA	960
OY	1198	CACCTATACATGCAATTCCTGTATTAACATGACCTCAGCCAGGAAACCAATTC	1257
Db	961	CATCCAAACATGCGGTACTTTGTGTATTAACATGATCTCAGCCCGGGAAACATTC	1020
OY	1258	GAATCCTTGTTCATCGTGTGTCAAACCACTGGAGATATGCAATGATCTGCAAGGGAG	1317
Db	1021	GAATCCTTGTTCATCAACATGTTTAAACCACTGCAATGATGATGTTCTGCAAGGGAA	1088
OY	1318	CAAGTTAACCTTCGGTATTTTACGGGTATTACTACGGTATACCAATCATGTTCTCT	1377
Db	1081	CAAGTTATCTTCGGTATTTTATGGGATTACTACGGTATCCCAACCATGTTCTCG	1144
OY	1378	TGATGAATCTTAAATTTGATTCACATTTCTGCAAGGACGTCAAGGTATGCTTACGAAAC	1437
Db	1141	GCTATGAATCTTAAATTTGATTCACATTTCTGCAAGGACGTCAAGGTATGCTTACGAAAC	1200
OY	1438	CAACATGATTTATTTGATCATCATATTAATCGGCTGGAAGAGAAAGGGGACAGCTCC	1497
Db	1201	CAGCATGATTTACTTTGATCATCATATTAATCGGCTGGAAGAGAAAGGGGATATGCTCC	1266
OY	1498	CACCCAAATTCAGGACTTGCACATTAATATGTCCGATGGGCCAGGGGGTATTAATATGAT	1557
Db	1261	CATCCAAATTCAGGACTTGCACCATTAATATGTCCAGATGGTCCAGGTGATTAACAAATGAT	1322
OY	1558	TATGTCCGGAAAACATTAAGCTGGCCAAATATGAGAGATATCACCGGAAATATGTTCTG	1617
Db	1321	TATGTGGGAAAAAATTAAGCCGGGACAAATTTGGAGAGATTAATTAACCGGAAATATGACA	1380
OY	1618	ACCGTACCATTAATGAGATGTTGGGGGAATTTCACTGTAAACGAGGGGCAATTTTC	1677
Db	1381	ACCGTACCAATTAATGAGAGATGTTGGGGTATTTCTCTGTAAATGAGGGGTCCTTTTC	1440

[illegible]

Db 241 ACAAGCAACAGCTACAGCTGGGTGACCTCTTTAAAAATAACGGCAATTCAGTATAT 300
Qy 538 GGGAGTGTCTGATGATCATTAAGGTGAGCAGACGGGACAGATGCTAAATGCGGTG 597
Db 301 GGTGATGTCTGATGATCATTAAGGTGAGCAGATGCTAAATGCTAAATGCGGTG 360
Qy 598 GAAGTGAACCGAAGCAACCGAAGCAAGAAATTCAGGTATACCATTTGAAGCATGG 657
Db 361 GAAGTGAATCGAAGCAACCGAAGCAAGAAATTCAGGTATACCATTTGAAGCATGG 420
Qy 658 ACGAAATTTGATTTCCCTGGAGAGGAAATACCATTTCAACTTTAAATGCGCTGTAT 717
Db 421 ACGAAATTTGATTTCCCTGGAGAGGAAATACCATTTCAACTTTAAATGCGCTGTAT 480
Qy 718 CATTTGATGGAGCAGATTGGGATTCAGTCACTGACGTTGAGAACAAATATTAATTC 777
Db 481 CATTTGATGGAGCAGATTGGGATTCAGTCACTGACGTTGAGAACAAATATTAATTC 540
Qy 778 AGAGGTACCGGAAGGATGGGACCTGGGAAGTGAATTAAGAACGGGCACTATGATTAC 837
Db 541 AGGGGAACAGGCAAGGCTGGAGCTGGAGAGTGAATTAAGAACGGGCACTATGATTAC 600
Qy 838 CTATGATGACAGACATTTGATGATCATCCAGAGTAATCAATGAATTTAGAAATTTG 897
Db 601 CTATGATGACAGACATTTGATGATCATCCAGAGTAATCAATGAATTTAGAAATTTG 660
Qy 898 GGAATTTGATTAACAATACATTAATCTAGATGATTTGAATTCGATGCTGGAACAT 957
Db 661 GGAATTTGATTAACAATACATTAATCTAGATGATTTGAATTCGATGCTGGAACAT 720
Qy 958 ATTAAATACAGCTATACAGAGATGGCTAAACATGGGTGAACCAAGGTAACCA 1017
Db 721 ATTAAATACAGCTATACAGAGATGGCTAAACATGGGTGAACCAAGGTAACCA 780
Qy 1018 ATGTTGACATGACAGATTTTGGAAAAATGACCTTGCTCAATTCGAAATCTATTTAAT 1077
Db 781 ATGTTGACATGCTGATGCTTTGGAAAAATGACCTTGCTCAATTCGAAATCTATTTAAT 840
Qy 1078 AAAACAAGTTGAATCACTCCGCTGCTGATGCTCTTCAATTAATTTGTAACATGCA 1137
Db 841 AAAACAAGTTGAATCACTCCGCTGCTGATGCTCTTCAATTAATTTGTAACATGCA 900
Qy 1138 TCTAATGCTGCTGCTATTTTGAATGAGAAATTTTAAATGCTGCTGTAACAAA 1197
Db 901 TCTAATGCTGCTGCTATTTTGAATGAGAAATTTTAAATGCTGCTGTAACAAA 960
Qy 1198 CACCTATACATGACATGATTTGTTGATTAACCATGACTCTGACCGAGAGAACTTG 1257
Db 961 CACCTATACATGACATGCTTTACTTTTGTGATTAACCATGACTCTGACCGAGAACTTG 1020
Qy 1258 GAATCTTTGTTCAATGCTGTTCAAAACACTGGCATATGATGATTTCTGACAGGAG 1317
Db 1021 GAATCTTTGTTCAATGCTGTTCAAAACACTGGCATATGATGATTTCTGACAGGAG 1080
Qy 1318 CAAGGTACCTTCCGATTTTAAAGGTGATTAACGATTAACCAATCAATGAGTCTT 1377
Db 1081 CAAGGTATCTTCCGATTTTAAAGGTGATTAACGATTAACCAATCAATGAGTCTT 1140
Qy 1378 TCGATGAATCTAAATTTGATCTGATGATTAATGCGCTGGAGAGAGAGGAGACGCTCC 1437
Db 1141 GCTATGAATCTAAATTTGATGATGATTAATGCGCTGGAGAGAGAGGAGAAATAGCTCC 1200
Qy 1438 CAACATGATTAATTTGATCATGATGATTAATGCGCTGGAGAGAGAGGAGACGCTCC 1497
Db 1201 CAGCATGATTAATTTGATCATGATGATTAATGCGCTGGAGAGAGAGGAGAAATAGCTCC 1260
Qy 1498 CACCAATTTCAAGACTTGAACATTAATGCGGATGGGCAAGGAGGATTAATTAATGATG 1557
Db 1261 CATCAATTTCAAGGCTTGGACCATTAATGCGGATGGGCAAGGAGGATTAATTAATGATG 1320
Qy 1558 TATGTGGGAAAACTAAAGCTGGCCAGATGAGAGATATCAACGGAAATAGGCTGTGT 1617
Db 1321 TATGTGGGAAAACTAAAGCTGGCCAGATGAGAGATATTAACGGAAATAGGACAGGC 1380

Qy 1618 ACCGTACCATTAATGACAGATGTTGGGAAATTTCACTGTAAACGAGGAGCAATTTG 1677
Db 1381 ACCGTACCATTAATGACAGATGTTGGGAAATTTCACTGTGTAAAGGAGGCTGTTGG 1440
Qy 1678 GTTGGGTGAAGCAA 1692
Db 1441 GTTGGGTGAAGCAA 1455

RESULT 14
US-10-327-837-9
; Sequence 9, Application US/10327837
; Publication No. US20030211958A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgaard-Frantzen Henrik
; APPLICANT: Outtrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: Novel -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/10/327,837
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: US/09/290,734
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Bacillus sp.
US-10-327-837-9

Query Match 65.7%; Score 1167; DB 17; Length 1455;
Best Local Similarity 87.6%; Pred. No. 4e-302;
Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

Qy 238 CATCATTAATGAGCAGATGGGACCATGATGACATTTTGAATGCAATTTGCCAAATGAC 297
Db 1 CATCATTAATGAGCAGATGGGACCATGATGACATTTTGAATGCAATTTGCCAAATGAC 60
Qy 298 GGAACACCTGGAACAGGTTTACGAGATGACGACCTTAACCTTAAGATTAAGGATTAAC 357
Db 61 GGAACATTTGGAACAGGTTTACGAGATGACGACCTTAACCTTAAGATTAAGGATTAAC 120
Qy 358 GCTGTTGATTTCTCTGCTGATGAGAGGGGACTTCCGAAATGATGTTGGTATGCTGCC 417
Db 121 GCTGTTGATTTCTCTGCTGATGAGAGGGGACTTCCGAAATGATGTTGGTATGAGGCC 180
Qy 418 TATGATTTGATGATTTGTTGATGATTTAAACAAAGGGAACGCTCGTACAAATATGCG 477
Db 181 TATGATTTGATGATTTGTTGATGATTTAAACAAAGGGAACGCTCGTACAAATATGCG 240
Qy 478 ACAAGAGTATGTTGCAAGGTGCGCTGATCATCTTTGAAATTAACGGGATTCAGTTTAT 537
Db 241 ACAAGAGTATGTTGCAAGGTGCGCTGATCATCTTTGAAATTAACGGGATTCAGTTTAT 300
Qy 538 GGGAGTGTGCTGATGATCATTAAGGTGAGCAGACGGGACAGAGATGTAATGCGGTG 597
Db 301 GGGAGTGTGCTGATGATCATTAAGGTGAGCAGACGGGACAGAGATGTAATGCGGTG 360
Qy 598 GAAGTGAACCGAAGCAACCGAAGCAAGAAATTCAGGTATACCATTTGAAGCATGG 657
Db 361 GAAGTGAATCGAAGCAACCGAAGCAAGAAATTCAGGTATACCATTTGAAGCATGG 420
Qy 658 ACGAAATTTGATTTCCCTGGAGAGGAAATACCATTTCAACTTTAAATGCGCTGTAT 717
Db 421 ACGAAATTTGATTTCCCTGGAGAGGAAATACCATTTCAACTTTAAATGCGCTGTAT 480
Qy 718 CATTTGATGGAGCAGATTGGGATTCAGTCACTGACGTTGAGAACAAATATTAATTC 777

481 CATTTGATGGACAGATTGGATAGTCACGCCGCTTCAAAACAAATATATTAATTC 540
 QY 778 AGAGTACCCGAAAGGCGATGGGACTGGGAGTATATAGAGACGGCACTATGATTAC 837
 Db 541 AGGGAAACAGCAAGGCGCTGGGACTGGGAGTATATAGAGATGGCACTATGACTAT 600
 QY 838 CTTATGATGAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 897
 Db 601 CTTATGATGAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
 QY 898 GAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 957
 Db 661 GAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
 QY 958 ATTAAATACAGCTATGAGAGATGGCTAAACATGTCGCTAACACCAAGGTAAACCA 1017
 Db 721 ATAAATATATACCTTATACAGAGATGGCTTACATGTCGCTAACACCAAGGTAAACCA 780
 QY 1018 ATGTTGAGTTGAGATTTTGGAAATAGACCTGCTGCAATCGAAATATTTAAT 1077
 Db 781 ATGTTGAGTTGAGATTTTGGAAATAGACCTGCTGCAATCGAAATATTTAAT 840
 QY 1078 AAAACAAGTTGGAATCACTCCGCTGCTGATGCTCTTCAATTAATTTGATACATGCA 1137
 Db 841 AAAACAAGTTGGAATCACTCCGCTGCTGATGCTCTTCAATTAATTTGATACATGCA 900
 QY 1138 TCTAATAGTGGCTATTTTGAATGAGAAATTTTAAATGTTCTGCTGCAAAA 1197
 Db 901 TCTAATAGTGGCTATTTTGAATGAGAAATTTTAAATGTTCTGCTGCAAAA 960
 QY 1198 CACCTTATACATGAGTACATTTGTTGATTAACATGCTGCTGCAAGGAGGAGCATG 1257
 Db 961 CACCTTATACATGAGTACATTTGTTGATTAACATGCTGCTGCAAGGAGGAGCATG 1020
 QY 1258 GAATCTTTTGTTCATCGTGGTCAAAACCACTGGCATATGATGATCTGCAAGGAG 1317
 Db 1021 GAATCTTTTGTTCATCGTGGTCAAAACCACTGGCATATGATGATCTGCAAGGAG 1080
 QY 1318 CAAGTTACCTTCCGCTATTTTACGCTGATTAATGCTGATTAACCACTGATGCTTCT 1377
 Db 1081 CAAGTTACCTTCCGCTATTTTACGCTGATTAATGCTGATTAACCACTGATGCTTCT 1140
 QY 1378 TCGATGAATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1437
 Db 1141 TCGATGAATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
 QY 1438 CAACATGATTTTGTTCATCATGATTAATGCTGCTGCAAGGAGGAGGAGCTCC 1497
 Db 1201 CAACATGATTTTGTTCATCATGATTAATGCTGCTGCAAGGAGGAGGAGGAGCTCC 1260
 QY 1498 CACCAATATGAGACTTGAACATTAATGCTGCTGCAAGGAGGAGGAGGAGGAGGAG 1557
 Db 1261 CACCAATATGAGACTTGAACATTAATGCTGCTGCAAGGAGGAGGAGGAGGAGGAG 1320
 QY 1558 TATGTCGGGAAACATTAAGCTGCGCAAGTATGAGAGATATCAACCGGAAATAGCTG 1617
 Db 1321 TATGTCGGGAAACATTAAGCTGCGCAAGTATGAGAGATATCAACCGGAAATAGCA 1380
 QY 1618 ACCGTCAACATTAATGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1677
 Db 1381 ACCGTCAACATTAATGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
 QY 1678 GTTGGGTGAGCA 1692
 Db 1441 GTTGGGTGAGCA 1455

RESULT 15
 US-10-327-837-14
 ; Sequence 14, Application US/10327837
 ; Publication No. US20030211958A1
 ; GENERAL INFORMATION:

APPLICANT: Svendsen, Allan
 APPLICANT: Borchert, Torben Vedel
 APPLICANT: Bisgaard-Brantzen Henrik
 APPLICANT: Outtrup, Helle
 APPLICANT: Nielsen, Bjarne Romfeldt
 APPLICANT: Nielsen, Vibeke Skovgaard
 APPLICANT: Hoeck, Lisbeth Hedegaard
 TITLE OF INVENTION: Novel -Amylase And -Amylase Mutants
 FILE REFERENCE: 5276,400-US
 CURRENT FILING DATE: 2002-12-23
 PRIOR APPLICATION NUMBER: US/09/290,734
 PRIOR FILING DATE: 1999-04-13
 NUMBER OF SEQ. ID NOS: 35
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 14
 LENGTH: 1455
 TYPE: DNA
 ORGANISM: Bacillus sp.
 US-10-327-837-14

Query Match 65.7%; Score 1167; DB 17; Length 1455;
 Best Local Similarity 87.6%; Pred. No. 4e-302;
 Matches 1275; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

238 CATCATATGAGAGAGATGGGACCATGATGATGATGATGATGATGATGATGATGATGAT 297
 Db 1 CATCATATGAGAGAGAGATGGGACCATGATGATGATGATGATGATGATGATGATGATGAT 60
 QY 298 GGAAGCACTGGAACAGGTTACGAGATGACGACGATTAATTAAGAGTAAAGGATTAAC 357
 Db 61 GGAAGCACTGGAACAGGTTACGAGATGACGACGATTAATTAAGAGTAAAGGATTAAC 120
 QY 358 GCTGTTGATCTCTCTGATGAGAGGAGCTTGCAGAAATGATGTTGGTATGTTGCC 417
 Db 121 GCTGTTGATCTCTCTGATGAGAGGAGCTTGCAGAAATGATGTTGGTATGTTGCC 180
 QY 418 TATGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 477
 Db 181 TATGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 QY 478 ACAAGAGTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 537
 Db 241 ACAAGAGTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
 QY 538 GGGGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 597
 Db 301 GGGGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
 QY 598 GAATGAGCAAGGAGCAACCGAAACCAAGAAATATCAGTGAATACACATTTGAAGCATG 657
 Db 361 GAATGAGTACGAGCAACCGAAACCAAGAAATATCAGTGAATACACATTTGAAGCATG 420
 QY 658 ACGAAATTTGATTTCTCTGGAAGAGAAATACCATTCCTCACTTAATGAGCGCTGAT 717
 Db 421 ACGAAATTTGATTTCTCTGGAAGAGAAATACCATTCCTCACTTAATGAGCGCTGAT 480
 QY 718 CATTTGATGAGACAGATTTGGATCAGTCACTGACCTTCAGAACAAATATATTAATTC 777
 Db 481 CATTTGATGAGACAGATTTGGATCAGTCACTGACCTTCAGAACAAATATATTAATTC 540
 QY 778 AGAGTACCGGAAAGGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 837
 Db 541 AGGGAAACAGCAAGGCTGGGACTGGGAGTGCATGACAGAGATGGCAACTATGACTAT 600
 QY 838 CTTATGATGAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 897
 Db 601 CTTATGATGAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
 QY 898 GAGATTTGATTAACAAATACATTAATCTGATGATGATGATGATGATGATGATGATGAT 957
 Db 661 GAGATGATGATTAACAAATACATTAATCTGATGATGATGATGATGATGATGATGATGAT 720

QY	958	ATTAAATACAGCTATACAGAGATTTGGCTAACACATGCGGTAAACACACAGGTAACCA	1017
Db	721	ATAAATAATATAGCTTTACAGAGATTTGGCTTAACATGTGGTAACACACAGGTAACCA	780
QY	1018	ATGTTTGCAGTTGCAGAAATTTTGGAAAAATGACCTTGCTCGATACGAAAACTATTTAAAT	1077
Db	781	ATGTTTGCAGTGGCTGAGTTTGGAAAAATGACCTTGCGTAATTTGAAAACTATTTGAAT	840
QY	1078	AAAACAAGTTGGAATCACTCCGTGTGCATGTCTCTCTTCAATTAATTTGTACATGCA	1137
Db	841	AAAACAAGTTGGAATCACTCCGTGTGTGATGTCTCTCTCACTTAATTTGTACAAAGCA	900
QY	1138	TCTAAATGTGGTGGCTATTTTGATATAGAAATTTTAAATGGTCTGTGTCACAAAA	1197
Db	901	TCTAATACCGGTGGTTATTAATGATGTAAGAAATTTTAAATGGTCTGTGTGCAAAAA	960
QY	1198	CACCTTAATACAGAGTCACATTTGTGTGTAACAACATGACTCTCAACCAAGAAAGCATTG	1257
Db	961	CATCCAAACATGCGCTTACTTTTGTGTATTAACATGATTTCTGACCCGGGGAAGCATTTG	1020
QY	1258	GAATCCTTTGTTCATTCGTGTTCAAACCACTGGCATATGCAATGATTTCTGACAAGGAG	1317
Db	1021	GAATCCTTTGTTCACAATATGTTTAAACCACTTGATATGCAATGTTCTGACAAGGAAA	1080
QY	1318	CAAGGTAAACCTTCCGTAATTTTAAAGGTATTAAGGTATACCAACTCATGTGTTCCCT	1377
Db	1081	CAAGGTATTCCTTCCGTAATTTTAAAGGTATTAAGGTATTAAGGTATTAAGGTATTAAGGT	1140
QY	1378	TGATGAATCTTAAATATGATTCACCTTGTGAGGACAGTCGTAACGTAATGCTTACGGAAC	1437
Db	1141	GCTAAGAAATCTTAAATATGAGACCTCTTGTGAGGACAGTCGTAACGTAATGCTTACG	1200
QY	1438	CAACATGATTTATTTGATCATGATATTAATCGGCTGAGAGAGAGAGGAGCAGCTCC	1497
Db	1201	CAGCATGATTTACTTTGATCATCATATTTAATCGGTTGAGACAGAGAGAGGAAATGCTCC	1260
QY	1498	CACCCAAATTCAGGACTTGGAACCTTATATGTCGATGAGGCCAGGGGGTATTAATGATG	1557
Db	1261	CATCCAAATTCAGGACTTGGAACCTTATATGATGATGATGATGATGATGATGATGATG	1320
QY	1558	TATGTGCGGGAACATTAAGCTGGCCAAATGATGAGAGATATCACCGGAAATAGTCTGAT	1617
Db	1321	TATGTGCGGGAACATTAAGCTGGGAACAATTTGAGAGATATTAACCGGAAATAGGACAGGC	1380
QY	1618	ACCGTACCATTAATGACAGATGTTGGGGGAATTTCACTGTAAACGAGGGGCACTTTCG	1677
Db	1381	ACCGTACCATTAATGACAGACGGAATGGGGTATTTCTGTTAATGAGAGGGTCCGTTTCG	1440
QY	1678	GTTTGGGTGAAGCAA	1692
Db	1441	GTTTGGGTGAAGCAA	1455

Search completed: May 2, 2005, 21:53:22
Job time : 730 secs

1	168.2	9.5	784	7	CF659180	CF659180	CCAH823TR
2	168.2	9.5	795	7	CF684098	CF684098	CCAGZ03TR
3	168.2	9.5	796	7	CF684188	CF684188	CCAE087TR
4	168.2	9.5	861	7	CF712259	CF712259	CCACX84TR
5	168.2	9.5	877	7	CF687730	CF687730	CCADZ24TR
6	168.2	9.5	888	7	CF675857	CF675857	CCADP57TR
7	168.2	9.5	889	7	CF6685247	CF6685247	CCALC87TR
8	163.2	9.2	773	7	CF6684810	CF684810	CCADG90TR
9	163.2	9.2	758	7	CF657851	CF657851	CCAGQ42TR
10	162.6	9.2	753	7	CF700043	CF700043	CCADG67TR
11	160.6	9.0	752	7	CF708585	CF708585	CCAGY26TR
12	141.8	8.0	727	7	CF717666	CF717666	CCAB472TR
13	136.8	7.7	741	7	CF705868	CF705868	CCAFJ84TR
14	126.2	7.1	856	8	CC131534	CC131534	NDL_49D22
15	124.6	7.0	576	8	BH377207	BH377207	AG-ND-109
16	103.8	5.8	534	8	BH379485	BH379485	AG-ND-124
17	97.6	5.5	885	7	CF685239	CF685239	CCALC87TR
18	96.8	5.5	652	7	CF643218	CF643218	D61_C12_F
19	96.8	5.5	689	7	CF642012	CF642012	D46_G07_F
20	95.4	5.4	685	6	CD488238	CD488238	D06_D07_T
21	90.8	5.1	428	5	BU539413	BU539413	mgcV413-KX
22	89.4	5.0	426	7	CF642668	CF642668	U54_E06_F
23	87.4	4.9	741	7	CF659170	CF659170	CCAH823TR
24	87.4	4.9	784	7	CF6597840	CF6597840	CCAGQ42TR

C	25	80.4	7	CF685993	CCAA811TF
C	26	87.4	4.9	CF684087	CCAG203TF
C	27	87.4	4.9	CF675860	CCADP57TF
C	28	87.4	4.9	CF717658	CCB4722TF
C	29	87.4	4.9	CF708576	CCAFY26TF
C	30	87.4	4.9	CF684179	CCABQ87TF
C	31	87.4	4.9	CF684804	CCADG90TF
C	32	87.4	4.9	CF712253	CCACY84TF
C	33	87.4	4.9	CF687718	CF687718
C	34	85.4	4.8	AU192670	CCADP24TF
C	35	83.8	4.7	AU192670	AU192670
C	36	82.8	4.7	CO148623	EST832831
C	37	82.8	4.7	CO138237	EST823676
C	38	82.2	4.6	BZ424843	EST832508
C	39	79.8	4.5	BUE640332	100020232
C	40	77.2	4.3	AU188840	mgcw019XO
C	41	77.2	4.3	CL945603	AU188400
C	42	76.2	4.3	CL945603	OSIF8B005
C	43	71.8	4.0	CF700027	CF700027
C	44	71.8	4.0	CD271159	CD271159
C	45	71.8	4.0	CO148015	EST823068
				CF644164	CF644164
					K17_F07 F

ALIGNMENTS

RESULT 1	CF699180	LOCUS	DEFINITION	ACCESSION
CF699180	784 bp	mRNA	linear	EST 16-AUG-2004
CCAH523TR	C. neoformans strain UBC21	Cryptococcus neoformans var. neoformans	CDNA clone CCAH523,	mRNA sequence.
CF699180				
CF699180.1	GI:41553339			

SOURCE	Cryptococcus neoformans var. neoformans (Filobasidiella neoformans var. neoformans)
ORGANISM	Cryptococcus neoformans var. neoformans

REFERENCE
1 (bases 1 to 784)

TITLE	End sequencing of clones from a Full length enriched, normalized

JOURNAL Unpublished (2003)

Contact: Brendan Loft

Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,

Tel: 301-838-3543

Email: crypto@tigr.org

Location/Qualifiers

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SOURCE
1. 1/81
/organism="Cryptococcus neoformans var. neoformans"

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/micr_type=illumina
/strain="JEC21"
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/usr/local/bin/canon: 70710
/clone="CCAH523"
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/chrome_11d=chrome11d
/note="Vector: pcmvsport6; Site 1: Not

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length; normalized ladder was prepared from a variety of conditions using RNA provided by Joseph Heitman and

ORIGIN

Query Match 9.5%; Score 168.2; DB 7; Length 784;

Matches 375; Conservative 0; Mismatches 323; Indels 3; Gaps 1;

259 ACCATGATGCAGTATTTTGAATGCCATTTGCCAAATGACGGGAACCACTGGAACAGTTA 318


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Db      70  ACAAATATGACGATCTTCGATGATGTCAGCTGAAGTGTGTGTATCAATTCGAAAAAGTAT 129
Qy      319 CGAGATGACGACGCTAATTAAAGAGTAAAGGATTAACCGCTGTTGGATTCCTCTGCA 378
Db      130 GAAAGCGMATCCGAAAGACTGCGCAACATGGGATCACTGCTGTTGATTCCTCTCTCT 189
Qy      379 TGAAGGGAATTCGCAAAATGATGTTGGGTATGTCCTTATATTTGTAACGATCTTGGT 438
Db      190 ACTAAAGGCTTAAGCCCTTAAGGGTACAGATATGATATTTATGATGTTGGGACTTGGGA 249
Qy      439 GAGTTTAACCAAAAGGAAACCGTCCGTACAAATATGSCACAAGAGTCAGTTGCAAGGT 498
Db      250 GAATTCGACCAAGAAAGATCTGTCCGTACCAATGGGGTACTAAGAAGATCTTTAAAA 309
Qy      499 GCCGTGACATCTTTGAAAAATTAACGGGATTCAGATTATGGGGATGTCGTGATGAATCAT 558
Db      310 GCATTTAAGGCTGCTTCTGGAAGGGCATTTATCACTGATGATGCTGCTTGAATTCAC 369
Qy      559 AAGGTGAGGACAGACGGGACAGAGATGTTAATGCCGTGGAAGTGAACGGAACCAACGA 618
Db      370 AAGGCCGCGCTGATGATTAAGAAATTTATGSCACCATGCTGAGACGAGATTAACCGT 429
Qy      619 AACCAAGAAATATCAGGTGAATACACCATTTGAAGCATGACGAAATTTGATTTCCCTGCA 678
Db      430 AACCAAGAAATAGAGAAATGACAAATTTGAAGGCTGACCAAGTTCACTTTCCCTGGC 489
Qy      679 AAGGAAATATCCATTCCTCACTTTAAATGSCGCTGATATCTTTGATGGGAACAGATTGG 738
Db      490 AAGGGGACACAGTACTCCGACATGAAGTGAATTTTAAACCATTTCAAGGGGTAGACT-- 547
Qy      739 GATCAGTACAGTCAAGCTTCAGAACAAATATATTAATTCAGAGTACCGGAAGGATGG 798
Db      548 -ATGACGCAAGACTGAGACACCGCTATCTTCAAGTTTAAGGGACGGAAACGATTGG 606
Qy      799 GACTGGAAATAGATATAGAGAACGGCACTATGATTAATCTTATGATGACAGATTGAT 858
Db      607 GCCACCGATGTTGATTAAGAAAACGGGCTTTGATTAATCTCATGTTTCCGATATTGAC 666
Qy      859 ATGAGATCATCAGAAATGATCAATGAACTTGAAGAAATGGGAGTTGGTATCAAAATACA 918
Db      667 CATTCACACCGGATGTTGAGGCCGAACTCAACAAATGGGGTAAATGGGTCTCCAAAGAG 726
Qy      919 CTTAATCTAGATGATTTAGATCGATGCTGTGAAACATAT 959
Db      727 ACAAATGCTTACGATTTCCGTTTCGACGCCGTCAACACAT 767

RESULT 2
CF684098 795 bp mRNA linear EST 16-AUG-2004
LOCUS CCAAG203TR C.neoformans strain JEC21 Cryptococcus neoformans var.
DEFINITION C.neoformans CDNA clone CCAAG203, mRNA sequence.
ACCESSION CF684098
VERSION CF684098.1 GI:41538257
KEYWORDS EST.
SOURCE Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
var. neoformans)
ORGANISM Cryptococcus neoformans var. neoformans
Bukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.
REFERENCE 1 (bases 1 to 795)
AUTHORS Loftus,B.
TITLE End sequencing of clones from a full length enriched, normalized
JEC21 cDNA library
JOURNAL Unpublished (2003)
COMMENT Other ESTs: CCAAG203TF
Contact: Brendan Loftus
TIGR Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-3543

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FEATURES
source
Location/Qualifiers
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/db_xref="taxon:40410"
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/notes="Vector: pCMVSPORT6; Site 1: NotI-EcoRV; The full
length, normalized library was prepared from a variety of
conditions using RNA provided by Joseph Heitman and
Jennifer Lodge"

ORIGIN
Query Match 9.5%; Score 168.2; DB 7; Length 795;
Best Local Similarity 53.5%; Pred. No. 2,2e-34;
Matches 375; Conservative 0; Mismatches 323; Indels 3; Gaps 1;

Qy      259 ACCATGATGACGATTTTGAATGCGATTTGCCAATGACGGGACACCTGGAACAGGTTA 318
Db      83 ACAAATGATCACTACTTCAATGATGACGCTGAAGGTGTGTGATGATTTGAAAAAGTAT 142
Qy      319 CGAGATGACGACGCTAATTAAAGAGTAAAGGATTAACCGCTGTTGGATTCCTCTGCA 378
Db      143 GAAAGGGAATCCGAAAGATGCGCAACATGGGCATCACTGCTGTTGATTCCTCTCTCT 202
Qy      379 TGAAGGGAATTCGCAAAATGATGTTGGGTATGTCCTATGATTTGTAACATCTTGGT 438
Db      203 ACTAAAGGCTTAAGCCCTTAAGGGTACAGGATGATGATTTATGATGTTGGGACTTGGGA 262
Qy      439 GAGTTTAACCAAAAGGAAACCGTCCGTACAAATATGSCACAAGAGTCAAGTTGCAAGGT 498
Db      263 GAATTCGACCAAGAAAGATCTGTCCGTACCAATGGGGTACTTAAGAGATCTTTAAAA 322
Qy      499 GCGGTGACATCTTTGAAAAATTAACGGGATTCAGTTTATGGGAGTCCGTGATGATCAT 558
Db      323 GCATTTAAGGCTGCTTCTGGAAGGGCATTTACAGTATGATGATGCTGTTGAATCAC 382
Qy      559 AAGGTGAGGACAGACGGGACAGAGATGTTAAATGCGGTGAAAGTGAACGGAACCAACGA 618
Db      383 AAGGCCGCGCTGATGATTAAGAAATTTATGSCACCATGCTGAGACGAGATTAACCGT 442
Qy      619 AACCAAGAAATATCAGGTGAATACACCATTTGAAGCATGACGAAATTTGATTTCCCTGCA 678
Db      443 AACCAAGAAATAGAGAAATGCAACACATTTGAAGGCTGACCAAGTTCACTTCCCTGGC 502
Qy      679 AAGGAAATACCAATTCCAACTTTAAATGCGCTGATCATTTTGTGATGGGACAGATTGG 738
Db      503 AAGGGGACAGATCTCCGACATGAAATGGAATTTTAAACATTTTCAAGGGTGAAGCT-- 560
Qy      739 GATCAGTCAAGTCAAGCTTCAAGCAAAATATTAATTCAGAGTACCGGAAGGATGG 798
Db      561 -ATGACGCAAGACTGAGACCAACCGCTATCTTCAAAATTCAGGGGACGGGAAGCATTTGG 619
Qy      799 GACTGGAAATAGATATAGAGAACGGCACTATGATTAATCTTATGATGACAGATTGAT 858
Db      620 GCCACCGATGATTAAGAAAGGCGGCTTTGATTAATCTCATGTTTCCGATATTGAC 679
Qy      859 ATGAGATCATCAGAAATGATCAATGAACTTGAAGAAATGGGAGTTGGTATCAAAATACA 918
Db      680 CATTCACACCGGATGTTGAGGCCAATCAACAAATGGGGTAAATGGGTCTCCCAAGAG 739
Qy      919 CTTAATCTAGATGATTTAGATCGATGCTGTGAAACATAT 959
Db      740 ACAAATGCTTACGATTTCCGTTTCGACGCCGTCAACACAT 780

RESULT 3
CF684188 796 bp mRNA linear EST 16-AUG-2004
LOCUS CF684188

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70 670

[illegible]

QY 499 GCCGTGACATCTTGAATAAAGGATTCAGTTTATGGGATGTCGATGATCAT 558
 Db 299 GCATTAAAGGCTCTTCTGAGAGGGCATTATACGTCATTAAGTGTCTTGAATCAC 358
 QY 559 AAGGTGAGCAGACGGGACAGAGATGTAATGCGGTGAGATGAAACCGAACCAACGA 618
 Db 359 AAGCGCGGCTGATGATTAAGAAATTAATGAGCCACATGATGAGCAGAAATACCGT 418
 QY 619 AACCAAGAAATATCAGGTGATATCACCATTTGAAGCATGACGAAATTTGATTTCCCTGGA 678
 Db 419 AACCAAGAAATGAGAAATGACCAACATTTGAAGGCTGAGCAAGTTCACTTTCCCTGGC 478
 QY 679 AGAGAAATACCCATTCACATTTAAATGCGCGGTGATCTTTGATGAGACAGATTGG 728
 Db 479 AGAGGCGACAGATCTCCGACATGAAATGTAATTTAACATTTTCACAGGGGATGACT-- 536
 QY 739 GATCAGTCAGTCAGCTTCAGAACAAATATATTAATTCAGAGGTACCGGAAAGGATGG 798
 Db 537 -ATGACGCAAAAGACTGAGACCAACCGCTATCTTCAAGATTCAGAGGGAGCAATGG 595
 QY 799 GATCGGGAATATATATGAGAACCGCACTATGATTAATCTTATGATGACATTTGAT 858
 Db 596 GCCACCGATGTTATTAAGAAACCGGCTCTTGCATTAATCTCATGTTTGCAGATATTGAC 655
 QY 859 ATGATCATCCAGAAATATCATGAACTTGAATTTGGGAGTTTGTATACAAATACA 918
 Db 656 CATTCACACCCGATGTTGAGCGCCGAACTCAACAAATGGGTAATGGTCTCCCAAGAG 715
 QY 919 CTTAATCTAGATGATTTAGAAATGATGATGCTGTGAAACATAT 959
 Db 716 ACAGTGCTCAGCTTCCGTTCCGTTTCAGAGCCGTCACAAACAT 756

RESULT 8 773 bp mRNA linear EST 16-AUG-2004
 CF684810
 LOCUS CCADG907R C.neoformans strain JEC21 Cryptococcus neoformans var.
 DEFINITION neoformans cDNA clone CCADG90, mRNA sequence.

ACCESSION CF684810
 VERSION CF684810.1 GI:41538969
 KEYWORDS EST.
 SOURCE Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
 var. neoformans)
 ORGANISM Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
 var. neoformans)
 Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
 Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
 Filobasidiella.
 1 (bases 1 to 773)

Loftus, B.
 TIGR
 JEC21 cDNA library
 Unpublished (2003)
 COMMENT Other ESTs: CCADG907F
 Contact: Brendan Loftus
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
 Rockville, MD 20850, USA
 Tel: 301-838-3543
 Fax: 301-838-0208
 Email: crypt@tigr.org
 Seg primer: TR.

FEATURES
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 /note="vector: pCMVSPORT6; Site_1: NotI EcoRV; The full
 length, normalized library was prepared from a variety of
 conditions using RNA provided by Joseph Heitman and

ORIGIN Jennifer Lodge"

Query Match 9.2%; Score 163.2; DB 7; Length 773;
 Best Local Similarity 54.3%; Pred. No. 5e-33;
 Matches 352; Conservative 0; Mismatches 293; Indels 3; Gaps 1;

QY 259 ACCATGATCAGATATTTGAATGGCATTTGCCAAATGAGGGGAACCATGAAACAGTTA 318
 Db 107 ACATATATGACATCTTCAATGATGTCGCTGAAGGTGGTGTGATTCATTGGAAAAATAT 166
 QY 319 CGAGATGACGACCTTAATTAAGAGTAAAGGATTAACCGCTGTTGATTCCTCTGCA 378
 Db 167 GAAGGAAATCCGAAAGATCGGCAACATGGGATCATGCTGTGATTCCTCTCT 226
 QY 379 TGAAGGGAATCTCGAAATATGATGGGTATGTCCTTAATGATTTGACATCTTGGT 438
 Db 227 ACTAAAGGCTTAAAGCCCTTAAGGATACAGATATGATTTATGATTTGGGACTTGGGA 286
 QY 439 GAGTTTAACCAAAAGGAAACCGTCCGTACAAATATGACACAAAGATCAGTTGCAAGGT 498
 Db 287 GAATTTGACCAAGAAAGATCTGTGCTTACCAATGGGGTACTTAAAGAAATCTTTAAAA 346
 QY 499 GCCGTGACATCTTTGAAAAATAACGGGATTCAGATTATGGGAGTGTCTGATGATCAT 558
 Db 347 GCATTAAGGCTGCTCTTGAGAAAGGCAATTATCAAGTATGATGATGCTGCTTGAATCAC 406
 QY 559 AAGGTGAGCAGACGGGACAGAGATGTAATGCGGTGAAAGTGAACCGAACCAACGA 618
 Db 407 AAGGCGGCGCTGATGATTAAGAAATTAATGAGCCACATGATGAGCAGAAATACCGT 466
 QY 619 AACCAAGAAATATCAGGTGATATACCATTTGAAGCATGAGCAAAATTTGATTTCCCTGGA 678
 Db 467 AACCAAGAAATGAGAAATGCAACATTTGAAGGTGAGCAAGTTCACTTTCCCTGGC 526
 QY 679 AAGGAAATACCCATTCACATTTAAATGCGCGGTGATCAATTTGATGGAGCAGATTGG 738
 Db 527 AGAGGCGACAGATCTCCGACATGAAATGGAATTTTAAACATTTTCAAGGGGTAGACTAT 586
 QY 739 GATCAGTCAGTCAGCTTCAGAACAAATATATTAATTCAGAGGTACCGGAAAGGATGG 798
 Db 587 GACGCAAAAGACTGAGACC--ACCGCTATCTTCAAGATTCAGAGGGAGCGGAAGCATGG 643
 QY 799 GACTGGGAATGATGATTAAGAACGGCACTATGATTAATCTTATGATGACAGATTTGAT 858
 Db 644 GCCACCGATGTTATTAAGAAACCGGCTCTTGCATTAATCTCATGTTTCCGATATTGAC 703
 QY 859 ATGATCATCCAGAAATATCATGAACTTGAATTTGGGAGTTGG 906
 Db 704 CATTCACACCCGATGTTGAGGCCGAACTCAACAAATGGGTTAAATGG 751

RESULT 9 798 bp mRNA linear EST 16-AUG-2004
 CF697851
 LOCUS CCAGQ427R C.neoformans strain JEC21 Cryptococcus neoformans var.
 DEFINITION neoformans cDNA clone CCAGQ42, mRNA sequence.

ACCESSION CF697851
 VERSION CF697851.1 GI:41552010
 KEYWORDS EST.
 SOURCE Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
 var. neoformans)
 ORGANISM Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
 var. neoformans)
 Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
 Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
 Filobasidiella.

Loftus, B.
 TIGR
 JEC21 cDNA library
 Unpublished (2003)
 COMMENT Other ESTs: CCAGQ427F
 Contact: Brendan Loftus

TIGR
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: crypt@tigr.org
Seq primer: TR.

FEATURES
SOURCE

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conditions using RNA provided by Joseph Heitman and
Jennifer Lodge"

ORIGIN

Query Match 9.2%; Score 163.2; DB 7; Length 798;
Best Local Similarity 54.3%; Pred. No. 5.1e-33;
Matches 352; Conservative 0; Mismatches 293; Indels 3; Gaps 1;

259 ACCATGATGCAATTTTGAATGCAATTTGCCAATGACCGGAACCACTGGAAACAGTTA 318
135 ACAATGATGCAATTTTGAATGCAATTTGCCAATGACCGGAACCACTGGAAACAGTTA 194
319 CGAGATGACGAGCTTAATTAAGATTAAGGATTAACCGCTGTTGATTCCTCTGCA 378
195 GAAAGCGAATCCGAAGACTGGCAACATGGGCACTGCTGTTGATTCCTCTGCA 254
379 TGAAGGGGACTTGGCAAAATGATGTTGGTATGCTTATGATTTGATGATCTTGGT 438
255 ACTAAGGCTCTACCCCTAAGGCTACAGATATGATTTATGATTTGATTTGGAATGGGA 314
439 GAGTTTAAACCAAAAGGGAACCGCTCGTACAAATATGACCAAGAGTCAATGCAACGT 498
315 GAATTCGACGAAAGATCTGTGCTGACCAATAGGGGTACTTAAAGATCTTTTAAA 374
499 GCCGTGACATCTTTGAAATAATTAACGGATTAACGTTATGGGATGCTGATGATCAT 558
375 GCATTAAGGCTGCTTGAAGAGGCAATTAACAGTATGATGATGCTGCTTGAATAC 434
559 AAAGGTGACGACGAGGACAGATGTTAATGCGTGAAGTGAACCGAAGCAACCGA 618
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619 AACCAAGAAATATGAGGATTAACCATTTGAAGATGAGCAAGAAATTTGATTTCCCTGGA 678
495 AACCAAGAAATATGAGGATTAACCATTTGAAGATGAGCAAGAAATTTGATTTCCCTGGA 554
679 AGAGGAATATCCCATTTCAATTAATGCGCTGATCAATTTGATGAGGACAGATGG 738
555 AGAGGCAACAGTACTCCGACATGATGAAATTTTAACTTTTCAACGAGGCTAGACTAT 614
739 GATCAGTACGCTGACCTTCAAGACAAATATATTAATTTCAAGATGACCGGAAGGATG 798
615 GAGCAAGAGTGAAC--ACCGTATCTTCAAGATTAAGGAGGAGGAGAGATGG 671
799 GACTGGGAATGATATGAGAGCGCACTATGATTTCTTATGATGACAGATGAT 858
672 GCCACCGATGTTGATTAAGAAAGGCTTTTCAATTTATCTCATGTTTGGCCGATATGAC 731
859 ATGATCATCCAGATTAATCAATGAATTTAGAAATGGGAGTTTG 906
732 CATTCACCCGAGTGTGAGCGGCACTCAACAAATGGGTTAATGG 779

RESULT 10
CF700043
LOCUS CF700043 793 bp mRNA linear EST 16-AUG-2004

DEFINITION CCADY677R C.neofomans strain JEC21 Cryptococcus neoformans var.
neoformans cDNA clone CCADY67, mRNA sequence.

ACCESSION CF700043
VERSION CF700043.1 GI:41554202

KEYWORDS

SOURCE EST.
Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
var. neoformans)

ORGANISM

Cryptococcus neoformans var. neoformans
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.
1 (bases 1 to 793)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

End sequencing of clones from a Full length enriched, normalized
JEC21 cDNA library
Unpublished (2003)
Other ESTs: CCADY67TF
Contact: Brendan Loftus
TIGR
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: crypt@tigr.org
Seq primer: TR.

FEATURES
SOURCE

1. 793
/organism="Cryptococcus neoformans var. neoformans"
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/db_xref="taxon:40410"
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length, normalized library was prepared from a variety of
conditions using RNA provided by Joseph Heitman and
Jennifer Lodge"

ORIGIN

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Best Local Similarity 54.4%; Pred. No. 7.4e-33;
Matches 349; Conservative 0; Mismatches 289; Indels 3; Gaps 1;

259 ACCATGATGCAATTTTGAATGCAATTTGCCAATGACCGGAACCACTGGAAACAGTTA 318
153 ACAATGATGCAATTTTGAATGCAATTTGCCAATGACCGGAACCACTGGAAACAGTTA 212
319 CGAGATGACGAGCTTAATTAAGATTAAGGATTAACCGCTGTTGATTCCTCTGCA 378
213 GAAAGCGAATCCGAAGACTGGCAACATGGGCACTGCTGTTGATTCCTCTGCA 272
379 TGAAGGGGACTTGGCAAAATGATGTTGGTATGCTTATGATTTGATGATCTTGGT 438
273 ACTAAGGCTCTACCCCTAAGGCTACAGATATGATTTATGATTTGATTTGGAATGGGA 332
439 GAGTTTAAACCAAAAGGGAACCGTCCGTAACAAATATGACACAGAGTCAATTTGCAAGT 498
333 GAATTCGACGAAAGATCTGTGCTGACCAAAATGAGGCTACTTAAAGAAATCTTTTAAA 392
499 GCCGTGACATCTTTGAAATAATTAACGGATTAACATTTATGAGGATGCTGATGATCAT 558
393 GCAATTAAGGCTGCTTGAAGAGGCAATTAACAGTATGATGATGCTGCTTGAATAC 452
559 AAAGGTGACGACGAGGACAGAGATGTAATCGGTGGAAGTGAACCGAAGCAACCGA 618
453 AAGCCGCGCTGATGATTAAGAAATTTATGCGCACATGCTGAGCAAGAAATTAACGT 512
619 AACCAAGAAATATGAGGATTAACCATTTGAAGATGAGCAAGAAATTTGATTTCCCTGGA 678
513 AACCAAGAAATATGAGGATTAACCATTTGAAGATGAGCAAGAAATTTGATTTCCCTGGA 572
679 AGAGGAATATCCCATTTCAATTAATGCGCTGATCAATTTGATGAGGACAGATGG 738

Db 573 AGAGGCGACAGTACTCCGACATGATGGAATTTTAACCATTTCAAGGGGTAGACT-- 630
QY 739 GATCACTGACGTAGCTTGGAACAAAATATTAATTCAGAGTACCGGAAGGATGG 798
Db 631 -ATGAGCGCAAGACTGAGACACCGCTATCTTCAAGATTCAGAGGAGCGGAAGCATTTGG 669
QY 799 GACTGGGAAGTATATAGAGAACGGCACTATGATTAATCTTATGATGAGACATTTGAT 858
Db 690 GCCACCGATTTATTAAGAAAACGGGTCTTTGATTTATCTCATGTTTGGCGATTTGAC 749
QY 859 ATGATCATTCAGAGTATCAATGAATTTAGAAATTTGGG 899
Db 750 CATTACACCCGATGTTGAGCCGAATCAACAAATGGGG 790

RESULT 11
CF708585 752 bp mRNA linear EST 16-AUG-2004
LOCUS CCAG4726TR C.neoformans strain JEC21 Cryptococcus neoformans var.
DEFINITION
ACCESSION CF708585
VERSION CF708585.1 GI:41562744
KEYWORDS EST.
SOURCE Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
var. neoformans)
ORGANISM Cryptococcus neoformans var. neoformans
Bukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.
1 (bases 1 to 752)
Loftus, B.
REFERENCE JEC21 cDNA library
AUTHORS Unpublished (2003)
COMMENT Other_ESTS: CCAG4726
Contact: Brendan Loftus
TIGR
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: crypt@tigr.org
Seq primer: TR.

FEATURES
source location/Qualifiers
1..752
/organism="Cryptococcus neoformans var. neoformans"
/mol_type="mRNA"
/strain="JEC21"
/db_xref="taxon:40410"
/clone="CCAG4726"
/note="Vector: pCMVSPORT6; Site 1: NotI EcoRV. The full
length, normalized library was prepared from a variety of
conditions using RNA provided by Joseph Heitman and
Jennifer Lodge"

ORIGIN
Query Match 9.0%; Score 160.6; DB 7; Length 752;
Best Local Similarity 54.3%; Pred. No. 2.6e-32;
Matches 347; Conservative 0; Mismatches 289; Indels 3; Gaps 1;
QY 259 ACCATGATGAGTATTTGAATGCAATTTGCCAAATGACGGGAACCACTGGAACAGTTA 318
Db 117 ACAATGATGAGTACTTGATGATGTAAGCGTGAAGTGTGTGATCACTTGGAAAAAGTAT 176
QY 319 CGAGATGACGACGCTAACTTAAAGATTAAGGATTAACGCTGTGTTGATTTCTCTCGCA 378
Db 177 GAAGAGGAATCCGAAGAGACTGGCCAAACATGGGCATCACTGCTGTGGATTCTCTCCCT 236
QY 379 TGAAGGGGAGCTTCGAAATGATGTTGGGTATGTCCTGATTTGTGATCTTGTGT 438
Db 237 ACTAAAGGCTTACCGCTAAGGGGTACAGGATATGATTTATGATGTTGGGACTTGGGA 296

QY 439 GAGTTTAACCAAAAGGAACCGTCCTGATACAAATATGCAAGAGTCAAGTTCAGAGT 498
Db 297 GATTTCGACGAGAAAGATCTGTCTGATACCAATGAGGTATCTTAAGAAATCTTTAAAA 356
QY 499 GCCGTGACATCTTTGAAAAATTAACGGGATTCAGATTATGAGGATGCTGTATGATCAT 558
Db 357 GCATTTAAGGCTGCTTCTGAGAAAGGCACTTATCACTGATGATGCTGCTTGAATCAC 416
QY 559 AAAGGTGAGCAGACGGGCAAGATGTAATGCGGTGAAAGTGAACCGAAGCAACCGA 618
Db 417 AAGCGCGGCTGATATTAAGAAAGATTTATGACCACATGCTGAGCAAGATTAACCGT 476
QY 619 AACCAAGAAATATCAGGTGAATACACATTTGAAGCAGTGAAGCAAAATTTATTCCTGGA 678
Db 477 AACAGGAAGTGAAGAAATGCAACAACTTGAAGCTGAGCAAGTCACTTTCCCTGGG 536
QY 679 AAGGAATATACCATTTCCAACTTTAATGCGGTGATCATTTTATGAGGACAGATTGG 738
Db 537 AGAGGCGACAGTACTCCGACATGAAATTTTAAACATTTCAAGGGGTAGACT-- 594
QY 739 GATCACTGACGTAGCTTGAGAAACAAATATTAATTCAGAGGTACCGGAAAGGATGG 798
Db 595 -ATGACGCAAGACTGAGACACCGCTATCTTCAAGATTCAGAGGAGCGGAAGCATTTGG 653
QY 799 GACTGGGAAGTATATAGAGAACGGCACTATGATTAATCTTATGATGAGACATTTGAT 858
Db 654 GCCACCGATGTTATTAAGAAAACGGGTCTTTGATTTATCTCATGTTTGGCGATTTGAC 713
QY 859 ATGATCATTCAGAGTATCAATGAATTTAGAAATTTGG 897
Db 714 CATTACACCCGATGTTGAGCCGAATCAACAAATGG 752

RESULT 12
CF717666 727 bp mRNA linear EST 16-AUG-2004
LOCUS CCAB4726R C.neoformans strain JEC21 Cryptococcus neoformans var.
DEFINITION
ACCESSION CF717666
VERSION CF717666.1 GI:41571825
KEYWORDS EST.
SOURCE Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
var. neoformans)
ORGANISM Cryptococcus neoformans var. neoformans
Bukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.
1 (bases 1 to 727)
Loftus, B.
REFERENCE JEC21 cDNA library
AUTHORS Unpublished (2003)
COMMENT Other_ESTS: CCAB4726
Contact: Brendan Loftus
TIGR
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: crypt@tigr.org
Seq primer: TR.

FEATURES
source location/Qualifiers
1..727
/organism="Cryptococcus neoformans var. neoformans"
/mol_type="mRNA"
/strain="JEC21"
/db_xref="taxon:40410"
/clone="CCAB4726"
/note="Vector: pCMVSPORT6; Site 1: NotI EcoRV. The full
length, normalized library was prepared from a variety of
conditions using RNA provided by Joseph Heitman and
Jennifer Lodge"

Seq primer: TR.

FEATURES	Location/Qualifiers
source	1. .741

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source
1. .741
/organism="Cryptococcus neoformans var. neoformans"
/mol type="mRNA"
/seq _1 "mRNA"
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/db_xref="taxon:40410"
/clone="CCAFU84"
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/clone_11b="C. neoformans strain JEC21"
 /note="Vector: pCMVSPORT6; Site 1: NotI EcoRV. The full
 length, normalized library was prepared from a variety of
 conditions using RNA provided by Joseph Heitman and
 Jennifer Lodge"

Query Match	7.7%	Score 136.8;	DB 7;	Length 741;
Best Local Similarity	53.0%	Pred. No. 8e-26;		
Matches 316;	Conservative	0;	Mismatches 277;	Indels 3;
			Gaps	1;

259 ACCATGATGCAGTATTTTGAATGGCATTTTGGCCAAATGACGGGAACCACTGGAAACAGGTTA 318

Db 144 ACAATGATCAGTACTTCGAATGGTACGCTGAAGGTGGTGTACATTGGAAAAAGTAT 203

319 CGAGATGACGACCTTAATTAAAGATAAGGATTACCGCTTTGGATTCTCTGCA 378

Db 204 GAAGCGATCCGAAGACTGGCCACATGGGCATCACTGCTGTGGATTCTCTCTCT 263

379 TGGAGGGGACTTCGCAAAATGATGTTGGGTATGTCCTATGATTTGTACGATCTTGGT 438

Db 264 ACTAAGCTCTAGCCCTAAGGCTACAGATATGATATTTATGATGTTGGGACTTGGGA 323

439 GAGTTTAAACCAAGGGAACCGTCGTAACAAATATGGCACAAGGAGTCAGTTGCAAGGT 498

Db 324 GAATTCGACGAGAAAGATCTGTGCTACCAATGGGGTACTTAAGAAGATCTTTTAAAA 383

499 GCCGTGACATCTTTGAAAAATAACGGATTCAAGTTTATGGGATGTCGTGATGAATCAT 558

Db 384 GCAATTAAAGGCTGCTTCTGAGAAGGCATTATCACGTACATTGATGCTGCTTGAATCAC 443

559 AAAGTGGACGACGCGACACAGATGTTAAATGCGGTGAAAGTGAAACCGAAGCAACCGA 618

Db 444 AAGCGCGCTGATGATTAAGAGAATTTATGCCACCATGTTGACGAGATTAACCGT 503

619 AACCAAGATATCAGGTGAATACACCAATGAAGCATGACGAATTGATTTCCCTGGA 678

Db 504 AACAGGAGTAGAGAATGCACACACTGAAGCTGGACCAATTCACTTCCCTGGC 563

679 AGAGGAAATACCCATTCCAACTTTAAATGCGCTGATCATTTTGATGGACAGATTGG 738

Db 564 AGAGCGCAAGTACTCGACATGAAGTCGAATTTTAAACCATTTCAACAGGGGTAGACT-- 621

739 GATCAGTCAGTCAGCTTCAGACAAAAATATATAATTACAGAGTACCGGAAAGGCATGG 798

Db 622 -ATGACGAAAGACTGAGACCA CGCTATCTTCAAGATTACGGGGGACGGGGAGCATTTGG 680

799 GACTGGAGTAGATATAGAGACGGCAACTATGATTACCTTATGTATGCAGACAT 854

Db 681 GCCACCGATGTTTGATAGAAAACGGTCTTTGCATATCTCATGTTGCCGATAT 736

RESULT 14
CC131534

LOCUS	856 bp	DNA	linear	GSS	16-APR-2003
CC131534					
DEFINITION	NDL.49D22.T7 Notre Dame Liverpool Aedes aegypti genomic clone				

NDL_49D22, genomic survey sequence.
CC131534

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VERSION      CC131534.1  GI:30000589
KEYWORDS     GSS.

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SOURCE	ORGANISM
Aedes aegypti (yellow fever mosquito)	Aedes aegypti
Aedes aegypti	Aedes aegypti

Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Eukaryota; Metazoa; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;

stegomyia.

REFERENCE
1 (bases 1 to 856)
Loftus, B., Shetty, J., Knudson, D. and Severson, D.
BAC end sequencing of *Aedes aegypti*
Unpublished (2003)
Other GSSs: NDL.49D22.SP6
Contact: Brendan Loftus
Department of Eukaryotic Genomics

TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: ent@tigr.org
Library was provided by David Severson
Seq primer: 17
Class: BAC ends.
Location/Qualifiers

FEATURES
source
1. .856
/organism="Aedes aegypti"
/mol_type="genomic DNA"
/strain="Liverpool"
/db_xref="taxon:7159"
/clone="NDL.49D22"
/note="Vector: pECRAC1; Site 1: Hind III; The library was prepared from whole body tissue of newly hatched L1 larvae by David Severson at the University of Notre Dame and Hongbin Zhang"

ORIGIN

Query Match 7.1%; Score 126.2; DB 8; Length 856;
Best Local Similarity 48.3%; Pred. No. 6.5e-23;

Matches 384; Conservative 0; Mismatches 408; Indels 3; Gaps 1;

624 AGAAATATCATGAGTATACCACTTGAAGCATGAGCAAAATTGATTTCCCTGGAAAGG 683
65 CATCTAGCAGCAGGAGCTTCAACCGCTGAGCTTACACCCGCTTCACTTTTCCGCGCTCA 124
684 AATATCCATTTCCAACTTTAAATGGCGCTGTATCATTTTGGATGGGACAGATTGGATCA 743
125 GGGCGTGATTCAGATTATCTGGATTCACATGCTTACGGCGCTGATTAAGTTGA 184
744 GTACGCTAGCTTCAAGAAACAAATATATTAATTCAG--GTACCGGAAAGCATGGGA 800
185 GCAGCCGAGCAGCAAGGGGTGTTCAAAATCGCCAGCACTATGCGCAGCGCTGGAA 244
801 CTGGAGATGATATATAGAAAGGCACTATGATTTACCTTATGATGACAGCAATGATAT 860
245 CGATCAGGTTGACGACAAAGGCACTACGACTATCTATGAGGGCCGACCTGGAGTT 304
861 GATCATCCAGAGTATCATGAACTTAAATAATTGGGAGTTTGTATCAAAATCACT 920
305 CCGCAATACCGCGCTGACGAGAGCTCAATACTGGCCCGCTGCTGTTGAAAGCCT 364
921 TAACTAGATGATTAGAAATGAGTGTGAAACATATTAATACGCTATACGAGAGA 980
365 GCGGTGAGCGGCTTCCGCTGAGCGCCAGCAATTCGCCCTGTTCTTCAAGA 424
981 TTGGCTAACATGTGGGTAAACACCAAGTAAACAAATGTTTGCAGTGCAGATTG 1040
425 GTGGCGGATCACGTGGCGGACGACGCGGACCTGTTATTTGTCCGAAATCTG 484
1041 GAAATATGACCTTGTCTGCAATTCGAAATCTATTTAAATATAAACAAGTTGATCACTCCGT 1100
485 GTGGCAGATCTGATGCTGCGTCAACATATCATGAGCTGTGACGCGCAAGGATGCT 544
1101 GTTCGATGTTCTCTCTATTAATATTTGTCATGATCATTAATAGTGTGCTATTTGA 1160
545 GTTCGAGTGGCGCTGACCTGAAGTTTATCATGAGCGCTCGAAACAGGGCGACGCTTGA 604

QY 1161 TATGAAATATTTTAAATGTTCTGTGTACAAAAACACCTATATACAGTACATTT 1220
DB 605 CATGGCGGATCTTTCACCGATACCTTACCGCCCGCATTCGGCCACGCGTACGCT 664
QY 1221 TCTTATTAACATGATCTGTACCGCAGAGAGACATTTGATCTTTGTTCAATCGTGT 1280
DB 665 GGTGCGCAACACGACACCCAGCCGTTGCAATCGCTGGAAGCGCGTGAACCTCTGTT 724
QY 1281 CAATCAGTGGATATGATTTATTTCTGACAAAGGAGAGAGTTACCTTCGTAATTTTA 1340
DB 725 CAACCGCTGGGCTTACGCGCTGATCTGTGCGCAACGAGCGCTGCTGCTGTTTGA 784
QY 1341 CGGTATTTACTACGG 1355
DB 785 CCCCAGCTGTATGG 799

RESULT 15
BH377207/c 576 bp DNA linear GSS 10-DEC-2001
LOCUS
DEFINITION AG-ND-109M22.TF ND-TM Anopheles gambiae genomic clone
AG-ND-109M22, genomic survey sequence.
ACCESSION BH377207
VERSION BH377207.1 GI:17323349
KEYWORDS
SOURCE
ORGANISM
Anopheles gambiae (African malaria mosquito)
Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
Anopheles.

REFERENCE
1 (bases 1 to 576)
Hong, Y.S., Hogan, J.R., Wang, X., Sarkar, A., Sim, C., Loftus, B., J.,
Ren, C., Huff, E.R., Carlisle, J.L., Black, K., Zhang, H.-B.,
Gardner, M.J., and Collins, F.H.

Construction of a BAC library and generation of BAC end
sequence-tagged connectors for genome sequencing of the African
malaria mosquito *Anopheles gambiae*
Mol. Genet. Genomics 268 (6), 720-728 (2003)

JOURNAL
MEDLINE
22542063
12653398
Other GSSs: AG-ND-109M22.TR
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjl@tigr.org

This clone is from an *A. gambiae* BAC library (ND-TM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from *A. gambiae* PEST strain
DNA. All DNA was extracted from DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&M University BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
partial digest.
Seq primer: M13 For
Class: BAC ends.
Location/Qualifiers

FEATURES
source
1. .576
/organism="Anopheles gambiae"
/mol_type="genomic DNA"
/strain="PEST"
/db_xref="taxon:7165"
/clone="AG-ND-109M22"
/clone_lib="ND-TM"
/note="Vector: pECRAC1; Site 1: HindIII"

ORIGIN

Query Match 7.0%; Score 124.6; DB 8; Length 576;
Best Local Similarity 52.4%; Pred. No. 1.6e-22;
Matches 297; Conservative 0; Mismatches 269; Indels 1; Gaps 1;

QY 421 GATTGTGACATCTTGTGAGTTTAACCAAGGGAACCGTCCGTACAAAATATGGACA 480
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 Db 576 GATTATTCGATTGAGAGATTATTCAGAAAGGAGATGTGCACCTAAATATGAACT 517
 |||||
 QY 481 AGGAGTCAGTTGCAAGGTCCGTGACATCTTGAATAAAGGATTCAAGTTATGGG 540
 |||||
 Db 516 AAGGAGATTATTTGGCCGTATATAACAGCTTAAGTAAGTAAAGTATTCAGATTATTGCA 457
 |||||
 QY 541 GATGTCGTGATGAAT-CATAAAGTGTGAGCAGACGGGACAGAGATGTAAATGCCGTGA 599
 |||||
 Db 456 GATATGTACTGAACCCATAAGCTGCGGTGACGAGCTGCAGAAATTCAGTTGTGGA 397
 |||||
 QY 600 AGTGAACCGAAGCAACGAAACCAAGAAATATCAGGTGAATACACCATTTGAAGCATGAGC 659
 |||||
 Db 396 AGTAAATCCGAAACCGAAATGAGTGCATCGAACCTTTATATTAATTAAGTCTTACAC 337
 |||||
 QY 660 GAAATTTGATTTCCCTGGAAGAGAAATACCATTCCAACCTTAAATGCGCTGTATCA 719
 |||||
 Db 336 GAAATTTATTTTCTGAGAGAAATPAGCAGATTCGGAATTTATCTGGATTTTACCTG 277
 |||||
 QY 720 TTTTGATGGGACAGTTGGGATCAGTCAGCTTCAGAACAAATATATTAATTGAG 779
 |||||
 Db 276 TTTTCAAGGTGTGAATGTGCTGAAGGAATTGATGTATGATATCGGGTATCAA 217
 |||||
 QY 780 AGTACCGGAAGGATGGGACTGGGAGTAGATATAGAAACGGCACTATGATTACCT 839
 |||||
 Db 216 TGATTATGAGATGTGGATGAAATTAATGATGATGAAAGGGAACTACGATTATCT 157
 |||||
 QY 840 TATGTATGACAGCATTTGATATGATCATCCAGAAATTAATCAATGAACTTAGAAATTTGGG 899
 |||||
 Db 156 GATGAATATATGATATAAATTTCCGAATCCAAATGTGTGGAGAAATTAGATTACTGGGG 97
 |||||
 QY 900 AGTTGGTATACAAATACACTTAATCTAGATGATTTGAATCGATGCTGTGAACATAT 959
 |||||
 Db 96 GAAAGTGTATATGAAACGATTTGATATATATGATATATGATATGATATGATATGATAT 37
 |||||
 QY 960 TAAATACAGCTATACGAGATTTGGCT 986
 |||||
 Db 36 TACACCGGCAATTTTAAAGACTGGCT 10
 |||||

Search completed: May 2, 2005, 20:14:17
 Job time : 4009 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 2, 2005, 19:07:27 ; Search time 77 Seconds
(without alignments)
2591.797 Million cell updates/sec

Title: US-08-952-741-2

Perfect score: 2862

Sequence: 1 MKLHNRIISVLTLLLAVAL.....ADGKGNFTVNGAIVSWVKQ 516

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: A_Geneseq_16Dec04:*

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1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2862	100.0	516	2	AAW11326 Alkaline
2	2862	100.0	516	5	AAE26535 Bacillus
3	2849	99.5	516	3	AAE35714 Mutant al
4	2713	94.8	485	5	AAO21000 Bacillus
5	2704	94.5	485	2	AAW79904 Bacillus
6	2613	91.3	485	2	AAW31499 Bacillus
7	2613	91.3	485	2	AAW48260 Bacillus
8	2613	91.3	485	2	AAW15421 Termauyl-
9	2613	91.3	485	2	AAW15415 Bacillus
10	2613	91.3	485	2	AAW25150 Bacillus
11	2613	91.3	485	2	AAW07391 Wild type
12	2613	91.3	485	2	AAW07381 Wild type
13	2613	91.3	485	3	AAW99602 Bacillus
14	2613	91.3	485	3	AAW99608 Bacillus
15	2613	91.3	485	5	AAE06933 Bacillus
16	2613	91.3	485	5	AAU12149 Bacillus
17	2613	91.3	485	5	AAE47850 Bacillus
18	2613	91.3	485	5	AAE47850 Bacillus
19	2613	91.3	485	6	AAE99480 Termauyl-
20	2613	91.3	485	7	AAJ92078 Termauyl-
21	2611	91.2	485	2	AAW12113 Alpha-amy
22	2610	91.2	485	2	AAW12121 Alpha-amy
23	2610	91.2	485	2	AAW12099 Alpha-amy
24	2610	91.2	485	2	AAW12130 Alpha-amy
25	2610	91.2	485	2	AAW12107 Alpha-amy

26	2610	91.2	485	2	AAW12119 Alpha-amy
27	2610	91.2	485	2	AAW12102 Alpha-amy
28	2610	91.2	485	2	AAW12108 Alpha-amy
29	2610	91.2	485	2	AAW12106 Alpha-amy
30	2610	91.2	485	2	AAW12129 Alpha-amy
31	2610	91.2	485	2	AAW12118 Alpha-amy
32	2610	91.2	485	2	AAW12098 Alpha-amy
33	2610	91.2	485	2	AAW12103 Alpha-amy
34	2610	91.2	485	2	AAW12104 Alpha-amy
35	2610	91.2	485	2	AAW12105 Alpha-amy
36	2610	91.2	485	2	AAW12120 Alpha-amy
37	2610	91.2	485	2	AAW12100 Alpha-amy
38	2609	91.2	485	2	AAW12114 Alpha-amy
39	2609	91.2	485	2	AAW12117 Alpha-amy
40	2608	91.1	485	2	AAW12122 Alpha-amy
41	2608	91.1	485	2	AAW12125 Alpha-amy
42	2608	91.1	485	2	AAW12124 Alpha-amy
43	2608	91.1	485	2	AAW12123 Alpha-amy
44	2608	91.1	485	2	AAW12126 Alpha-amy
45	2608	91.1	485	2	AAW12131 Alpha-amy

ALIGNMENTS

RESULT 1
AAW11326 standard; protein; 516 AA.
XX
AC AAW11326;
XX
DT 17-OCT-2003 (revised)
DT 27-AUG-2003 (revised)
DT 11-NOV-1997 (first entry)
XX
DE Alkaline liquefying alpha-amyase.
XX
KW Alkaline liquefying alpha-amyase; Bacillus; alpha-amyase; detergent;
KW starch-related polysaccharide; hydrolase; enzyme; surfactant resistance;
KW alpha-1,4-glucosidic link; alkalophilic Bacillus; laundry detergent;
KW dish-washing detergent; starch.
XX
OS Bacillus sp; KSM-AP1378.
XX
XX W09700324-A1.
XX
XX 03-JAN-1997.
XX
XX 14-JUN-1996; 96WO-JP001641.
XX
XX 14-JUN-1995; 95JP-00147257.
XX
XX (KAOS) KAO CORP.
XX
XX Hatada Y, Ozaki K, Ara K, Kawai S, Ito S;
XX WPI; 1997-118708/11.
XX DR N-PSDB; AAT51339.
XX
XX DNA encoding alkaline liquefying alpha-amyase - useful in dish-washing
XX PT and laundry detergents for removal of starch dirts.
XX
XX Claim 2; Page 23-26; 40pp; English.
XX
XX This sequence represents an alkaline liquefying alpha-amyase. Alpha-
XX amyase is an enzyme that acts on starch-related polysaccharides,
XX hydrolysing the alpha-1,4-glucoside bond of the polysaccharide molecule.
XX Alkaline liquefying alpha-amyases exhibit resistance to surfactants used
XX in detergents, and decompose starch or starch-related polysaccharides in
XX a highly random manner. The Bacillus species KSM-AP1378, from which this
XX sequence was isolated, is an alkalophilic Bacillus strain. It was
XX isolated from soil in the vicinity of the city of Tochihi. The enzyme is
XX useful in improving the efficiency of dish-washing and laundry

CC detergents, particularly on starch dirts. (Updated on 27-AUG-2003 to
CC correct OS field.) (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 516 AA;

Query Match 100.0%; Score 2862; DB 2; Length 516;
Best Local Similarity 100.0%; Pred. No. 8.1e-226;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCLHNRIISVLTLLAVALFPYMTPEAOAHNNGTNGTMMQYFEWHLPRDGNHNRRLD 60
DB 1 MCLHNRIISVLTLLAVALFPYMTPEAOAHNNGTNGTMMQYFEWHLPRDGNHNRRLD 60
QY 61 DAANLKSQGITAWIPPAWKGTSONDVGAYDLYDLGEFNOKGTVRTKYGTSQLOQAV 120
DB 61 DAANLKSQGITAWIPPAWKGTSONDVGAYDLYDLGEFNOKGTVRTKYGTSQLOQAV 120
QY 121 TSLKNNGIOYGGDVVNMHKGADGTEMVNAVEVNSNRNOEISGEYTIEMTKFDPGRG 180
DB 121 TSLKNNGIOYGGDVVNMHKGADGTEMVNAVEVNSNRNOEISGEYTIEMTKFDPGRG 180
QY 181 NTHSNFKRWYHFDGTDWDOSROLQNKIKYFRGTGKAMDEVDIENGNDYLMYADIDMD 240
DB 181 NTHSNFKRWYHFDGTDWDOSROLQNKIKYFRGTGKAMDEVDIENGNDYLMYADIDMD 240
QY 241 HPEVINELRWGWYNTNTLNDGFRIDAVKHIKYSTYRDLTHVRNTTGKPMFAVAEFMK 300
DB 241 HPEVINELRWGWYNTNTLNDGFRIDAVKHIKYSTYRDLTHVRNTTGKPMFAVAEFMK 300
QY 301 NDIAAIENTYLNKTSNMHNSVDFDPLHYNLYNASNSGGYFDMRNILNGSVQKPIHAATFV 360
DB 301 NDIAAIENTYLNKTSNMHNSVDFDPLHYNLYNASNSGGYFDMRNILNGSVQKPIHAATFV 360
QY 361 DNHDSPGELALBESFVQSWFKPLAYALILTRREGQPSVFYGDYGIPTHGVPSSKSIDPL 420
DB 361 DNHDSPGELALBESFVQSWFKPLAYALILTRREGQPSVFYGDYGIPTHGVPSSKSIDPL 420
QY 421 LOAROTYAYGTOHDYDPHDDIIGMTREGDSSHNSGLATIMSDPGGNKMMYVQKHAQ 480
DB 421 LOAROTYAYGTOHDYDPHDDIIGMTREGDSSHNSGLATIMSDPGGNKMMYVQKHAQ 480
QY 481 VWRDITGNRSQGVTTINADGWNFTVNGAVSVWVKQ 516
DB 481 VWRDITGNRSQGVTTINADGWNFTVNGAVSVWVKQ 516

RESULT 2
AAE26535
ID AAE26535 standard; protein; 516 AA.

XX
AC AAE26535;
DT 13-DEC-2002 (first entry)

XX
DE Bacillus species KSM-AP1378 alpha-amylase protein.

XX
KM alpha amylase; alpha-1,4-glucan-4-glucanohydrolase; EC 3.2.1.1;
KW dishwashing; textile desizing; detergent; paper; starch liquefaction;
KM laundry; alcohol production; ethanol production; pulp; beer; brewing;
XX
KM sweetener; enzyme.

OS Bacillus sp.

XX
FH Key Location/Qualifiers

FT Peptide 1..31

FT Protein /label= Signal-peptide
32..516
/note= "Mature KSM-AP1378 protein"

XX
PN W0200231124-A2.

XX
PD 18-APR-2002.

PF 12-OCT-2001; 2001WO-DK000668.
XX
XX 13-OCT-2000; 2000DK-00001533.
PR 23-OCT-2000; 2000US-0242692P.
PR 02-OCT-2001; 2001DK-00001442.
PR 03-OCT-2001; 2001US-0326752P.

XX
PA (NOVO) NOVOZYMES AS.

XX
PI Andersen C;

XX
XX WPI; 2002-463264/49.

DR N-PSDB; AAD4364.

XX
XX KSM-K36 or KSM-K38 variant from Bacillus for cleaning dishes, textile
PT desizing, starch liquefaction and ethanol production has alpha-amylase
PT activity.

PS Disclosure; Page 64-66; 69pp; English.

XX
XX The present invention relates to KSM-K36 or KSM-K38 variant of parent
CC alpha-amylases (alpha-1,4-glucan-4-glucanohydrolases, EC 3.2.1.1) from
CC Bacillus. The variants have alpha-amylase activity and exhibit an amino
CC acid alteration such as an insertion, deletion or substitution of the
CC parent alpha-amylase. The variants are useful for washing and/or dish-
CC washing, textile desizing, starch liquefaction and alcohol production,
CC particularly ethanol production. They are also useful as components in
CC detergents for e.g. laundry, dishwashing and hard surface cleaning
CC detergent compositions, in pulp and paper production, in beer making or
CC brewing and in production of sweeteners. The present sequence is Bacillus
CC species KSM-AP1378 alpha-amylase protein
XX

SQ Sequence 516 AA;

Query Match 100.0%; Score 2862; DB 5; Length 516;
Best Local Similarity 100.0%; Pred. No. 8.1e-226;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCLHNRIISVLTLLAVALFPYMTPEAOAHNNGTNGTMMQYFEWHLPRDGNHNRRLD 60
DB 1 MCLHNRIISVLTLLAVALFPYMTPEAOAHNNGTNGTMMQYFEWHLPRDGNHNRRLD 60
QY 61 DAANLKSQGITAWIPPAWKGTSONDVGAYDLYDLGEFNOKGTVRTKYGTSQLOQAV 120
DB 61 DAANLKSQGITAWIPPAWKGTSONDVGAYDLYDLGEFNOKGTVRTKYGTSQLOQAV 120
QY 121 TSLKNNGIOYGGDVVNMHKGADGTEMVNAVEVNSNRNOEISGEYTIEMTKFDPGRG 180
DB 121 TSLKNNGIOYGGDVVNMHKGADGTEMVNAVEVNSNRNOEISGEYTIEMTKFDPGRG 180
QY 181 NTHSNFKRWYHFDGTDWDOSROLQNKIKYFRGTGKAMDEVDIENGNDYLMYADIDMD 240
DB 181 NTHSNFKRWYHFDGTDWDOSROLQNKIKYFRGTGKAMDEVDIENGNDYLMYADIDMD 240
QY 241 HPEVINELRWGWYNTNTLNDGFRIDAVKHIKYSTYRDLTHVRNTTGKPMFAVAEFMK 300
DB 241 HPEVINELRWGWYNTNTLNDGFRIDAVKHIKYSTYRDLTHVRNTTGKPMFAVAEFMK 300
QY 301 NDIAAIENTYLNKTSNMHNSVDFDPLHYNLYNASNSGGYFDMRNILNGSVQKPIHAATFV 360
DB 301 NDIAAIENTYLNKTSNMHNSVDFDPLHYNLYNASNSGGYFDMRNILNGSVQKPIHAATFV 360
QY 361 DNHDSPGELALBESFVQSWFKPLAYALILTRREGQPSVFYGDYGIPTHGVPSSKSIDPL 420
DB 361 DNHDSPGELALBESFVQSWFKPLAYALILTRREGQPSVFYGDYGIPTHGVPSSKSIDPL 420
QY 421 LOAROTYAYGTOHDYDPHDDIIGMTREGDSSHNSGLATIMSDPGGNKMMYVQKHAQ 480
DB 421 LOAROTYAYGTOHDYDPHDDIIGMTREGDSSHNSGLATIMSDPGGNKMMYVQKHAQ 480
QY 481 VWRDITGNRSQGVTTINADGWNFTVNGAVSVWVKQ 516
DB 481 VWRDITGNRSQGVTTINADGWNFTVNGAVSVWVKQ 516

RESULT 3
ID AAB35714 standard; protein; 516 AA.
XX AAB35714;
AC AAB35714;
DT 19-FEB-2001 (first entry)
XX
DE Mutant alpha-amylase amino acid sequence.
XX
KM Alpha-amylase; detergent; Bacillus.
XX
OS Bacillus sp.
XX
FH Key Location/Qualifiers
FT Misc-difference 297
FT /note= "Represented as Alu in the specification"
FT Misc-difference 335
FT /note= "Represented as Aly in the specification"
XX
PN JP2000245466-A.
XX
PD 12-SEP-2000.
XX
PF 25-FEB-1999; 99JP-00048213.
XX
PR 25-FEB-1999; 99JP-00048213.
XX
PA (KAOS) KAO CORP.
XX
DR WPI: 2000-615143/59.
DR N-PSDB; AAC66234.
XX
PT A novel mutant alpha-amylase for use in a detergent composition.
XX
PS Claim 1; Page 5-6; 12pp; Japanese.
XX
CC The present invention relates to a mutant alpha-amylase. Included in the
CC invention are a gene encoding the mutant alpha-amylase, a vector
CC containing the gene, and a transformed cell recombined by the vector. The
CC enzyme is used in a detergent composition. The present sequence
CC represents the mutant alpha-amylase protein
XX
SQ Sequence 516 AA:
Query Match 99.5%; Score 2849; DB 3; Length 516;
Best Local Similarity 99.6%; Pred. No. 9.4e-225;
Matches 514; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MCLNRIISVLLTLLAVAVLPYMTTEPAQAHNNGTGMQYFEMHLPNDGNHNRIRD 60
DB 1 MCLNRIISVLLTLLAVAVLPYMTTEPAQAHNNGTGMQYFEMHLPNDGNHNRIRD 60
QY 61 DAALAKSGTAAWIIPAMKGTSONDVGYGAYDIYDLGEFQKGTGRTKYSQLOGAV 120
DB 61 DAALAKSGTAAWIIPAMKGTSONDVGYGAYDIYDLGEFQKGTGRTKYSQLOGAV 120
QY 121 TSLKNGNIOYVGDVVMNHKGGADGTEMVNAVEVNRNSRNOEISGEYTIETATKFPDPRG 180
DB 121 TSLKNGNIOYVGDVVMNHKGGADGTEMVNAVEVNRNSRNOEISGEYTIETATKFPDPRG 180
QY 121 TSLKNGNIOYVGDVVMNHKGGADGTEMVNAVEVNRNSRNOEISGEYTIETATKFPDPRG 180
DB 121 TSLKNGNIOYVGDVVMNHKGGADGTEMVNAVEVNRNSRNOEISGEYTIETATKFPDPRG 180
QY 181 NTHSNFPMRWYHFDGTWDQSRQLNKIKYKRGTKAMDEVDIENGNYDYLAADIDMD 240
DB 181 NTHSNFPMRWYHFDGTWDQSRQLNKIKYKRGTKAMDEVDIENGNYDYLAADIDMD 240
QY 181 NTHSNFPMRWYHFDGTWDQSRQLNKIKYKRGTKAMDEVDIENGNYDYLAADIDMD 240
DB 181 NTHSNFPMRWYHFDGTWDQSRQLNKIKYKRGTKAMDEVDIENGNYDYLAADIDMD 240
QY 241 HPEVINELRMNGVWYTTNLNIGFRIDAVKIKSYTRDMLTHTVNTTGKMEFAVAFWK 300
DB 241 HPEVINELRMNGVWYTTNLNIGFRIDAVKIKSYTRDMLTHTVNTTGKMEFAVAFWK 300
QY 301 NDLAIAINYLKITSWNHSEVDFVPLAHYNLYNASNKGYPDMENILNGSVQKPIHAYTFV 360
DB 301 NDLAIAINYLKITSWNHSEVDFVPLAHYNLYNASNKGYPDMENILNGSVQKPIHAYTFV 360

DB 301 NDLAIAINYLKITSWNHSEVDFVPLAHYNLYNASNKGYPDMENILNGSVQKPIHAYTFV 360
QY 361 DNHSOPGEALIESFVQSMFKPLAVALILTRQGYPSVFGYGIPTHGVPMSKIDPL 420
DB 361 DNHSOPGEALIESFVQSMFKPLAVALILTRQGYPSVFGYGIPTHGVPMSKIDPL 420
QY 421 LQARQYAYGTQHDYFPHHDIIGWTRGDSHPNSGLATTIMSDPGGNKMYTVGKHRAQ 480
DB 421 LQARQYAYGTQHDYFPHHDIIGWTRGDSHPNSGLATTIMSDPGGNKMYTVGKHRAQ 480
QY 481 VMRDITGNRSGTGTINADGWNFTVNGGAVSVWVK 516
DB 481 VMRDITGNRSGTGTINADGWNFTVNGGAVSVWVK 516
RESULT 4
ID AAO21000 standard; protein; 485 AA.
XX AAO21000;
AC AAO21000;
DT 19-JUL-2002 (first entry)
XX
DE Bacillus sp alpha-amylase KSM-API378 (FERM BP-3048) protein.
XX
KM Alpha-amylase; detergent; laundry; bleaching; dishwashing; enzyme;
KM fibre desizing; starch liquefaction; KSM-API378; FERM BP-3048.
XX
OS Bacillus sp.
XX
FH Key Location/Qualifiers
FT Protein 1..485
FT /note= "Mature protein"
XX
PN EPI199356-A2.
XX
PD 24-APR-2002.
XX
PF 10-OCT-2001; 2001EP-00123378.
XX
PR 11-OCT-2000; 2000JP-00310605.
XX
PA (KAOS) KAO CORP.
XX
PI Araki H, Hagihari H, Hayashi Y, Endo K, Igarashi K, Ozaki K;
XX
DR WPI: 2002-354203/39.
DR N-PSDB; AAK99881.
XX
PT New mutant alpha-amylase, useful in detergent compositions, comprises
PT increased productivity when prepared recombinantly and better resistance
PT to heat.
XX
PS Claim 1; Page 16-18; 45pp; English.
XX
CC The invention relates to a mutant alpha-amylase derived from a fully
CC defined sequence of 485 amino acids or a 480 aa sequence as given in the
CC specification by substitution or deletion of one or more specified amino
CC acids. The mutant amylase proteins of the invention can be produced at a
CC high yield from a recombinant organism, making it possible to drastically
CC reduce the cost of their production. The mutant amylase proteins are
CC useful in detergent compositions (e.g. laundry, bleaching and dishwashing
CC compositions), also for liquefaction of starch and desizing fibres,
CC optionally used in conjunction with other enzymes. This sequence
CC represents the 485 amino acid Bacillus sp. alpha-amylase KSM-API378 (FERM
CC BP-3048) protein of the invention
XX
SQ Sequence 485 AA:
Query Match 94.8%; Score 2713; DB 5; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.2e-213;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 HHNGTGMQVYEMHLPNDGNHNRRLRDDAANKSKGITAIVWIPRPMKGTSONDVGGA 91
 DB 1 HHNGTGMQVYEMHLPNDGNHNRRLRDDAANKSKGITAIVWIPRPMKGTSONDVGGA 60
 QY 92 YDLIDGEPNOKGTAVTKYGTGTSQLOQAVTSLKNNGIQYVGVVNMHKGADGTEWNAV 151
 DB 61 YDLIDGEPNOKGTAVTKYGTGTSQLOQAVTSLKNNGIQYVGVVNMHKGADGTEWNAV 120
 QY 152 EVNRSNRNOEISGEYTIEMWTKFDPGRGNTSHNFKRWYHFDGTDQSRQLOKNTIYK 211
 DB 121 EVNRSNRNOEISGEYTIEMWTKFDPGRGNTSHNFKRWYHFDGTDQSRQLOKNTIYK 180
 QY 212 RGTGKAMDWEVDIENGNYDYLMYADIDMDHPEYINELRMGWYTYTTLNDGFRIDAVKH 271
 DB 181 RGTGKAMDWEVDIENGNYDYLMYADIDMDHPEYINELRMGWYTYTTLNDGFRIDAVKH 240
 QY 272 IKSYTRDMLTHVRNTTGKMPFAVAEFWKNDLAIENYLNKTSWNHSEVDPPLHYNL 331
 DB 241 IKSYTRDMLTHVRNTTGKMPFAVAEFWKNDLAIENYLNKTSWNHSEVDPPLHYNL 300
 QY 332 SNGGYFDMENIINGSVQKHPHIAVTFVNDHDSQGEALSFVQSWFKPLAYALLITRE 391
 DB 301 SNGGYFDMENIINGSVQKHPHIAVTFVNDHDSQGEALSFVQSWFKPLAYALLITRE 360
 QY 392 OGYPVYFGDYGIPTHGVPMSKIDPLLOARQTYAGTGHYFPHHDIIGWTRGDS 451
 DB 361 OGYPVYFGDYGIPTHGVPMSKIDPLLOARQTYAGTGHYFPHHDIIGWTRGDS 420
 QY 452 HPMNSGLATIMSDPGGNKMYVGVKHAQVWRDITGNRSGVTITNDGWNFTVNGAVS 511
 DB 421 HPMNSGLATIMSDPGGNKMYVGVKHAQVWRDITGNRSGVTITNDGWNFTVNGAVS 480
 QY 512 VVWKQ 516
 DB 481 VVWKQ 485

RESULT 5
 AAM79904
 ID AAM79904 standard; protein; 485 AA.
 XX
 AC AAM79904;
 XX
 DT 18-DEC-1998 (first entry)
 XX
 DE Liquefied alkaline alpha-amylase.
 XX
 KM Liquefied alkaline alpha-amylase; mutation; Bacillus licheniformis;
 XX
 KM detergent; bleaching agent; oxidising agent.
 XX
 OS Bacillus licheniformis.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 202
 FT /note= "can be deleted or substituted by another amino
 acid residue such as Thr, Ile, Leu, Ala, Val or Ser"

XX WO9844126-A1.
 XX 08-OCT-1998.
 XX PF 31-MAR-1998; 98WO-JP001464.
 XX PR 31-MAR-1997; 97JP-00080299.
 XX (KAOS) KAO CORP.
 XX PI Hatada Y, Ikawa K, Ito S;
 XX WPI; 1998-542707/46.
 XX DR
 XX PT Bacillus derived alpha amylase having mutation at position 202 - has
 PT optimum pH in alkaline conditions and high tolerance to oxidants, useful

PT for production of detergent compositions.
 XX
 XX Claim 1; Page 19-21; 42pp; Japanese.
 XX
 CC The present sequence represents Bacillus licheniformis liquefied alkaline
 CC alpha-amylase. The present invention describes mutated forms of the
 CC liquefied alkaline alpha-amylase derived from Bacillus species KSM-AP1378
 CC (FERM BP-3048), having the methionine residue at position 202 either
 CC deleted or substituted by another amino acid, such as threonine,
 CC isoleucine, leucine, alanine, valine or serine. The mutated enzyme may
 CC have other mutations (such as deletion of arginine or glycine at
 CC positions 181 and 182, respectively) but at least 95.28 homologous to the
 CC original enzyme. The mutated enzyme has optimum pH in alkaline
 CC conditions, a high alpha amylase activity, and a high and sustained
 CC tolerance to oxidising substances. The enzyme may be used in the
 CC formulation of liquid, powder or granular detergent compositions,
 CC especially those containing bleaches and oxidants. The enzyme retains
 CC high activity in the presence of bleaches and oxidants allowing improved
 CC detergent formulations to be produced
 XX

SO Sequence 485 AA;
 Query Match 94.5%; Score 2704; DB 2; Length 485;
 Best Local Similarity 99.8%; Pred. No. 6,7e-213;
 Matches 484; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 32 HHNGTGMQVYEMHLPNDGNHNRRLRDDAANKSKGITAIVWIPRPMKGTSONDVGGA 91
 DB 1 HHNGTGMQVYEMHLPNDGNHNRRLRDDAANKSKGITAIVWIPRPMKGTSONDVGGA 60
 QY 92 YDLIDGEPNOKGTAVTKYGTGTSQLOQAVTSLKNNGIQYVGVVNMHKGADGTEWNAV 151
 DB 61 YDLIDGEPNOKGTAVTKYGTGTSQLOQAVTSLKNNGIQYVGVVNMHKGADGTEWNAV 120
 QY 152 EVNRSNRNOEISGEYTIEMWTKFDPGRGNTSHNFKRWYHFDGTDQSRQLOKNTIYK 211
 DB 121 EVNRSNRNOEISGEYTIEMWTKFDPGRGNTSHNFKRWYHFDGTDQSRQLOKNTIYK 180
 QY 212 RGTGKAMDWEVDIENGNYDYLMYADIDMDHPEYINELRMGWYTYTTLNDGFRIDAVKH 271
 DB 181 RGTGKAMDWEVDIENGNYDYLMYADIDMDHPEYINELRMGWYTYTTLNDGFRIDAVKH 240
 QY 272 IKSYTRDMLTHVRNTTGKMPFAVAEFWKNDLAIENYLNKTSWNHSEVDPPLHYNL 331
 DB 241 IKSYTRDMLTHVRNTTGKMPFAVAEFWKNDLAIENYLNKTSWNHSEVDPPLHYNL 300
 QY 392 OGYPVYFGDYGIPTHGVPMSKIDPLLOARQTYAGTGHYFPHHDIIGWTRGDS 451
 DB 361 OGYPVYFGDYGIPTHGVPMSKIDPLLOARQTYAGTGHYFPHHDIIGWTRGDS 420
 QY 452 HPMNSGLATIMSDPGGNKMYVGVKHAQVWRDITGNRSGVTITNDGWNFTVNGAVS 511
 DB 421 HPMNSGLATIMSDPGGNKMYVGVKHAQVWRDITGNRSGVTITNDGWNFTVNGAVS 480
 QY 512 VVWKQ 516
 DB 481 VVWKQ 485

RESULT 6
 AAM31499
 ID AAM31499 standard; protein; 485 AA.
 XX
 AC AAM31499;
 XX
 DT 08-APR-1998 (first entry)
 XX
 DE Bacillus sp. alpha amylase.
 XX

KW Alpha amylase; hard surface cleaning; dishwashing; laundry.
 XX Bacillus sp.
 XX WO9732961-A2.
 XX 12-SEP-1997.
 XX 04-MAR-1997; 97WO-US003635.
 XX 07-MAR-1996; 96WO-US003276.
 XX (PROC) PROCTER & GAMBLE CO.
 XX Baec AC, Jones LA, Ohtani R, Pramod K, Rai S, Showell MS;
 XX Ward G;
 XX WPI; 1997-457524/42.
 XX Detergent compositions for hard surface cleaning and laundry use -
 XX PT contains Bacillus derived alpha amylase with improved thermostability,
 XX PT reduced calcium ion dependency etc.
 XX Claim 1; Page 86-87; 97pp; English.
 XX The present sequence is a Bacillus sp. alpha amylase with a specific
 XX activity at least 25% higher than that of Termamyl (RTM) at 25 to 55
 XX degrees C at pH 8 to 10, measured by the Phadebas (RTM) activity test. It
 XX is of use in hard surface cleaning, hand or machine dishwashing and
 XX laundry at a temperature of 10 to 25 degrees C. Improved cleaning, stain
 XX removal and fabric care are obtained by using it at a concentration of
 XX 0.00018 to 0.06%
 XX Sequence 485 AA;
 XX SQ

Query Match 91.3%; Score 2613; DB 2; Length 485;
 Best Local Similarity 95.1%; Pred. No. 1.9e-205;
 Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

QY 32 HHNGTNGTMQYFEMHLPNDGNHNRRLRDDAANKSKGITAVWIPPAWKGSQNDVGYGA 91
 DB 1 HHNGTNGTMQYFEMHLPNDGNHNRRLRDDAANKSKGITAVWIPPAWKGSQNDVGYGA 60
 QY 92 YDLVLDGFBFNOGKTVRTKYGTRSOLOGAVTSLKNNGIQVGDVYNNHKGADGTEBMNAV 151
 DB 61 YDLVLDGFBFNOGKTVRTKYGTRNOLOAAVTSLKNNGIQVGDVYNNHKGADGTEIYNAV 120
 QY 152 EVNSNRNOISGEXTIEAMTKFDPFGKGNTHSNFKRWYHFDGTDMDQSOLOKNIYKF 211
 DB 121 EVNSNRNOISGEXTIEAMTKFDPFGKGNTHSNFKRWYHFDGTDMDQSOLOKNIYKF 180
 QY 212 RGTGKAMDWEVDIENGAVDYLMYADIMDHPVINELRNKGWVYNTNLNDGFRIDAVKH 271
 DB 181 RGTGKAMDWEVDIENGAVDYLMYADIMDHPVINELRNKGWVYNTNLNDGFRIDAVKH 240
 QY 272 IKYSTRTDLTHVNTTGGKPMFAVAEFWKNDLAAIENYLNKTSWNHVSFDPVPLHYNLYNA 331
 DB 241 IKYSTRTDLTHVNTTGGKPMFAVAEFWKNDLAAIENYLNKTSWNHVSFDPVPLHYNLYNA 300
 QY 332 SNSGGYFDMRNILNGSVVQKPHIAVTFVNDHDSQPEALSSFYQSWFKPLAYALITRE 391
 DB 301 SNSGGYFDMRNILNGSVVQKPHIAVTFVNDHDSQPEALSSFYQSWFKPLAYALITRE 360
 QY 392 QGYPSVFGDYGGIPTHGVPMSKSIDPLLOARQTYAVGTQHDYFDHDDIIGWTREGDSS 451
 DB 361 QGYPSVFGDYGGIPTHGVPMSKSIDPLLOARQTYAVGTQHDYFDHDDIIGWTREGDSS 420
 QY 452 HPNSGLATIMSDGPGKNTVGVKHKAGQVWRDITGNSSGVTITNADQWGFYNGGAVS 511
 DB 421 HPNSGLATIMSDGPGKNTVGVKHKAGQVWRDITGNSSGVTITNADQWGFYNGGAVS 480
 QY 512 VVWVXQ 516
 DB |||||

DB 481 VVWVXQ 485

RESULT 7
 AAW48260
 ID AAW48260 standard; protein; 485 AA.

AAW48260;
 02-JUL-1998 (first entry)

Bacillus sp. alpha amylase protein #1.

Alpha amylase; stain digestion; detergent; fabric laundry performance.

Bacillus sp.

WO9805748-A1.

12-FEB-1998.

01-AUG-1996; 96WO-US012612.

01-AUG-1996; 96WO-US012612.

(PROC) PROCTER & GAMBLE CO.

Baek AC, Jones LA, Ohtani R, Pramod K, Rai S, Showell MS;

WPI; 1998-159168/14.

Use of specific alpha-amylase enzymes - in laundry detergent compositions
 to provide effective cleaning and whitening of dingy fabrics.

Claim 1; Page 69-70; 82pp; English.

This sequence represents an alpha amylase from Bacillus sp. which is used
 in a laundry detergent. The detergent compositions can be used for
 boosting fabric laundry performance or for dingy fabric cleanup

Sequence 485 AA;

Query Match 91.3%; Score 2613; DB 2; Length 485;
 Best Local Similarity 95.1%; Pred. No. 1.9e-205;
 Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

QY 32 HHNGTNGTMQYFEMHLPNDGNHNRRLRDDAANKSKGITAVWIPPAWKGSQNDVGYGA 91
 DB 1 HHNGTNGTMQYFEMHLPNDGNHNRRLRDDAANKSKGITAVWIPPAWKGSQNDVGYGA 60
 QY 92 YDLVLDGFBFNOGKTVRTKYGTRSOLOGAVTSLKNNGIQVGDVYNNHKGADGTEBMNAV 151
 DB 61 YDLVLDGFBFNOGKTVRTKYGTRNOLOAAVTSLKNNGIQVGDVYNNHKGADGTEIYNAV 120
 QY 152 EVNSNRNOISGEXTIEAMTKFDPFGKGNTHSNFKRWYHFDGTDMDQSOLOKNIYKF 211
 DB 121 EVNSNRNOISGEXTIEAMTKFDPFGKGNTHSNFKRWYHFDGTDMDQSOLOKNIYKF 180
 QY 212 RGTGKAMDWEVDIENGAVDYLMYADIMDHPVINELRNKGWVYNTNLNDGFRIDAVKH 271
 DB 181 RGTGKAMDWEVDIENGAVDYLMYADIMDHPVINELRNKGWVYNTNLNDGFRIDAVKH 240
 QY 272 IKYSTRTDLTHVNTTGGKPMFAVAEFWKNDLAAIENYLNKTSWNHVSFDPVPLHYNLYNA 331
 DB 241 IKYSTRTDLTHVNTTGGKPMFAVAEFWKNDLAAIENYLNKTSWNHVSFDPVPLHYNLYNA 300
 QY 332 SNSGGYFDMRNILNGSVVQKPHIAVTFVNDHDSQPEALSSFYQSWFKPLAYALITRE 391
 DB 301 SNSGGYFDMRNILNGSVVQKPHIAVTFVNDHDSQPEALSSFYQSWFKPLAYALITRE 360
 QY 392 QGYPSVFGDYGGIPTHGVPMSKSIDPLLOARQTYAVGTQHDYFDHDDIIGWTREGDSS 451
 DB 361 QGYPSVFGDYGGIPTHGVPMSKSIDPLLOARQTYAVGTQHDYFDHDDIIGWTREGDSS 420

OY		452	HPSGLATIMSDGPGSKMMVYGKKGQWVRDITGNRSGFVTINADGMNPTVVGSAVS	511
Db		421	HPNSGLATIMSDGPGSKMMVYGKKGQWVRDITGNRTGVITINADGMNFVSNGSVS	480
OY		512	VWVKQ 516	
Db		481	VWVKQ 485	
RESULT 8				
ID	AAV15421			
AC	AAV15421 standard; protein; 485 AA.			
XX	AAV15421;			
XX				
DT	22-JUL-1999 (first entry)			
XX				
DE	Termamyl-like alpha-amylase protein.			
KM	Termamyl-like; alpha-amylase; variant; washing; dishwashing; production;			
KW	sweetener; ethanol; starch; textile desizing; starch liquefaction;			
XX	saccharification process.			
OS	Bacillus sp.			
XX				
PM	MO9923211-A1.			
XX				
PD	14-MAY-1999.			
XX				
PF	30-OCT-1998; 98WO-DK000471.			
XX				
PR	30-OCT-1997; 97DK-00001240.			
PR	14-JUL-1998; 98DK-00000936.			
XX				
PA	(NOVO) NOVO-NORDISK AS.			
XX				
Pt	Borchert TV, Svendsen A, Andersen C, Nielsen BR, Nissen TL;			
PI	Kjaerulf S;			
XX				
DR	WPI, 1999-326987/27.			
XX				
PT	New Termamyl-like alpha-amylase variants.			
XX				
PS	Claim 38; Page 88-89; 115pp; English.			
CC	The specification describes termamyl-like alpha-amylase variants that			
CC	have altered amino acid sequences to improve properties. The variants are			
CC	produced by creating one or more of the following mutations in amino acid			
CC	sequences of the parent termamyl-like alpha-amylase: T141, K142, F143,			
CC	D144, F145, P146, G147, R148, G149, Q174, R181, G182, D183, G184, K185,			
CC	A186, M189, S193, N195, H107, K108, G109, D166, W167, D168, Q169, S170,			
CC	R171, Q172, F173, F267, W268, K269, N270, D271, L272, G273, A274, L275,			
CC	K311, E346, K385, G456, N457, K458, P459, G460, T461, V462, T463. The			
CC	variants can be used for washing and/or dishwashing. They can also be			
CC	used in the production of sweeteners and ethanol from starch, and/or for			
CC	textile desizing, and in starch liquefaction and/or saccharification			
CC	processes. The present amylase can function as the parent sequence in the			
CC	production of the variants of the invention			
SQ	Sequence 485 AA;			

	Query Match	Similarity	Score	DB 2	Length	485	
Best Local	461	95.1%	Pred. No. 1	9e-205			
Matches	461	Conservative	16	Mismatches	8	Indels	0
QY	32	HHNGNGTMMQYFEMFLPNDGSHHNRRLRDDANLNSKGTITAWIPRPMGTGSDNDGYGA	91				
DB	1	HHNGNGTMMQYFEMFLPNDGSHHNRRLRDDANLNSKGTITAWIPRPMGTGSDNDGYGA	60				
QY	92	YDLVYDLGEFNQKGTATTKYTGTSQLOGAVTSLKNNGIQYGGDVVNMHKGADGTEVMVAV	151				
DB	61	YDLVYDLGEFNQKGTATTKYTGTSQLOGAVTSLKNNGIQYGGDVVNMHKGADGTEVMVAV	120				

OY	152	EVNNSNNRQELSGEYTLLEAMTKRPPGGKGNTHSNKMRWHYHDDGDMQSRQLQKIYKF	211
Db	121	EVNNSNNRQETSGEYALEAMTKRPPGGKGNHSSKMRWHYHDDGDMQSRQLQKIYKF	180
OY	212	RGTKKAMDWEVDINGNNDYLMYADIDMDHPEVINELRNMGVWYTNLTNLDFRIDAVKH	271
Db	181	RGTKKAMDWEVDITENGNDYLMYADVDMDHPEVIHELNRMGVWYTNLTNLDFRIDAVKH	240
OY	272	IKSYETRDMLTHYKNTTKCKPFAVAEFKKNLLAALENTLNKTSNMHSVEDVPLHYNLVA	331
Db	241	IKSYETRDMLTHYKNTTKCKPFAVAEFKKNLLGALENTLNKTSNMHSVEDVPLHYNLVA	300
OY	332	SNNGGYFPMRNILINGSVVOKKPIHAYTFVDNDHSDSGEALSESFYOSWEKPLAYALLTRE	391
Db	301	SNNGGYFPMRNILINGSVVOKKPIHAYTFVDNDHSDSGEALSESFYOSWEKPLAYALLTRE	360
OY	392	QGYSVFYGDYVYGIPTHGVPMSKSKIDPILQARQTYAVGTQHDYVDHDIIGWTREGDSS	451
Db	361	QGYSVFYGDYVYGIPTHGVPMSKSKIDPILQARQTYAVGTQHDYVDHDIIGWTREGDSS	420
OY	452	HPNSGLATIMSDGPGKKNMYVGGKKAQVWRDITGNSSGYTTINADGNGFTVNGAYS	511
Db	421	HPNSGLATIMSDGPGKKNMYVGGKKAQVWRDITGNRTGYTTINADGNGFTVNGAYS	480
OY	512	VWVKQ 516	
Db	481	VWVKQ 485	
RESULT 9			
AA15415			
ID	AA15415	standard; protein; 485 AA.	
XX	AA15415;		
XX	22-JUL-1999	(first entry)	
DE	Bacillus strain NCIB 12512	alpha-amylase protein.	
XX			
XX	Termamyl-like; alpha-amylase; variant; washing; diehawing; production;		
KW	sweetener; ethanol; starch; textile desizing; starch liquefaction;		
KW	saccharification process.		
XX			
OS	Bacillus sp.		
XX			
PN	WO9923211-A1.		
XX			
PD	14-MAY-1999.		
XX			
PF	30-OCT-1998;	98WO-DK000471.	
XX			
PR	30-OCT-1997;	97DK-00001240.	
PR	14-JUL-1998;	98DK-00000936.	
XX			
PA	(NOVO) NOVO-NORDISK AS.		
PI	Borchert TV, Svendsen A, Andersen C, Nielsen BR, Nissen TL;		
PI	Kjaerulff S;		
XX			
DR	WPI, 1999-326987/27.		
XX			
PT	New Termamyl-like alpha-amylase variants.		
XX			
PS	Claim 38; Page 77-79; 115pp; English.		

CC K311, E346, K385, G456, N457, K458, P459, G460, T461, V462, T463. The
 CC variants can be used for washing and/or dishwashing. They can also be
 CC used in the production of sweeteners and ethanol from starch and/or for
 CC textile desizing, and in starch liquefaction and/or saccharification
 CC processes. The present amylase can function as the parent sequence in the
 CC production of the variants of the invention

XX Sequence 485 AA;

Query Match 91.3%; Score 2613; DB 2; Length 485;
 Best Local Similarity 95.1%; Pred. No. 1.9e-205;
 Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

QY 32 HHNGNGTMMQYFEEHLLPNDGNHNRRLDDAANKSKGITA VWPAAKGTSONDVGCA 91
 DB 1 HHNGNGTMMQYFEEHLLPNDGNHNRRLDDAANKSKGITA VWPAAKGTSONDVGCA 60
 QY 92 YDLVLDGEFNQKGTVRTKYGTSRQLQCAVTSKNNNGIOYGDVVMNHHKGADGTEMVAV 151
 DB 61 YDLVLDGEFNQKGTVRTKYGTSRQLQCAVTSKNNNGIOYGDVVMNHHKGADGTEMVAV 120
 QY 152 EVNRSNRNOEISGEYTIEMATKFDPPGRGNTHSNFKRWYHFDGTDMDQSRLQNKIKYF 211
 DB 121 EVNRSNRNOEISGEYTIEMATKFDPPGRGNTHSNFKRWYHFDGTDMDQSRLQNKIKYF 180
 QY 212 RGTGKAMWEDVDIENGNDYLMYADIDMDHEVINELRNMGVWYNTNTLNDGFRIDAVKH 271
 DB 181 RGTGKAMWEDVDIENGNDYLMYADIDMDHEVINELRNMGVWYNTNTLNDGFRIDAVKH 240
 QY 272 IKYSTRLDMLTHVNTTGKPMFAVAEFWKNDLAIENYLNKTSNMHSYFDVPLHNLVNA 331
 DB 241 IKYSTRLDMLTHVNTTGKPMFAVAEFWKNDLAIENYLNKTSNMHSYFDVPLHNLVNA 300
 QY 332 SNSGGEYFDMRNILNGSVVQKHPHATVVDNHDSDPGBALSFVQSWFKPLAVALITRE 391
 DB 301 SNSGGEYFDMRNILNGSVVQKHPHATVVDNHDSDPGBALSFVQSWFKPLAVALITRE 360
 QY 392 OGYSVFEYGDYVGLPTHGVPMSKSIDPLQARQTYAAGTODYFDHDDIIGWTRREGSS 451
 DB 361 OGYSVFEYGDYVGLPTHGVPMSKSIDPLQARQTYAAGTODYFDHDDIIGWTRREGSS 420
 QY 452 HPNSGLATIMSDGPGNKMVYVGGKAKGQVWRDITGNRSQVTITNADGNGFTVNGAVS 511
 DB 421 HPNSGLATIMSDGPGNKMVYVGGKAKGQVWRDITGNRSQVTITNADGNGFTVNGAVS 480
 QY 512 VVWKQ 516
 DB 481 VVWKQ 485

RESULT 10
 AAY25150
 ID AAY25150 standard; protein; 485 AA.

XX AC AAY25150;

XX DT 27-AUG-1999 (first entry)

XX DE Bacillus sp. alpha-amylase protein fragment 1.

XX KM Alpha-amylase; cleaning composition; protease variant; spot removal;
 KM detergent composition; hard surface cleaning; fabric cleaning;
 KM dishwashing composition; oral cleaning composition; personal cleansing;
 KM stain removal; soil removal; whiteness maintenance; dingy cleanup;
 KM film removal.

XX KM Bacillus sp.

XX OS WO9920723-A2.

XX XX 29-APR-1999.

XX PF 23-OCT-1998; 98WO-US022486.

XX 23-OCT-1997; 97US-00956323.
 PR 23-OCT-1997; 97US-00956324.
 PR 23-OCT-1997; 97US-00956554.
 XX (PROC) PROCTER & GAMBLE CO.

PI Ghosh CK, Baack AC, Ohtani R, Busch A, Showell MS;

DR WPI; 1999-404706/34.

PT Cleaning compositions used in e.g. detergent for cleaning hard surfaces
 PT or fabrics, dishwashing or oral cleaning comprises protease and amylase
 PT variants having amino acid residues.

PS Claim 1b(11); Page 164-165; 169pp; English.

CC This invention describes novel cleaning compositions which contain a
 CC protease variant with an amino acid substitution corresponding to
 CC position 103 of Bacillus amyloliquefaciens and an alpha-amylase variant.
 CC The compositions can be used in e.g. detergent compositions, for cleaning
 CC hard surfaces or fabrics, dishwashing compositions, oral cleaning
 CC compositions, detergent cleaning compositions and personal cleansing
 CC compositions. The combination of protease variants and alpha-amylase
 CC variants in cleaning compositions can provide improved and enhanced
 CC cleaning ability, including stain and/or soil removal and/or reduction
 CC and/or whiteness maintenance and/or dingy cleanup and/or spot and/or film
 CC removal and/or reduction, over conventional enzyme-containing cleaning
 CC compositions

XX Sequence 485 AA;

Query Match 91.3%; Score 2613; DB 2; Length 485;
 Best Local Similarity 95.1%; Pred. No. 1.9e-205;
 Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

QY 32 HHNGNGTMMQYFEEHLLPNDGNHNRRLDDAANKSKGITA VWPAAKGTSONDVGCA 91
 DB 1 HHNGNGTMMQYFEEHLLPNDGNHNRRLDDAANKSKGITA VWPAAKGTSONDVGCA 60
 QY 92 YDLVLDGEFNQKGTVRTKYGTSRQLQCAVTSKNNNGIOYGDVVMNHHKGADGTEMVAV 151
 DB 61 YDLVLDGEFNQKGTVRTKYGTSRQLQCAVTSKNNNGIOYGDVVMNHHKGADGTEMVAV 120
 QY 152 EVNRSNRNOEISGEYTIEMATKFDPPGRGNTHSNFKRWYHFDGTDMDQSRLQNKIKYF 211
 DB 121 EVNRSNRNOEISGEYTIEMATKFDPPGRGNTHSNFKRWYHFDGTDMDQSRLQNKIKYF 180
 QY 212 RGTGKAMWEDVDIENGNDYLMYADIDMDHEVINELRNMGVWYNTNTLNDGFRIDAVKH 271
 DB 181 RGTGKAMWEDVDIENGNDYLMYADIDMDHEVINELRNMGVWYNTNTLNDGFRIDAVKH 240
 QY 272 IKYSTRLDMLTHVNTTGKPMFAVAEFWKNDLAIENYLNKTSNMHSYFDVPLHNLVNA 331
 DB 241 IKYSTRLDMLTHVNTTGKPMFAVAEFWKNDLAIENYLNKTSNMHSYFDVPLHNLVNA 300
 QY 332 SNSGGEYFDMRNILNGSVVQKHPHATVVDNHDSDPGBALSFVQSWFKPLAVALITRE 391
 DB 301 SNSGGEYFDMRNILNGSVVQKHPHATVVDNHDSDPGBALSFVQSWFKPLAVALITRE 360
 QY 392 OGYSVFEYGDYVGLPTHGVPMSKSIDPLQARQTYAAGTODYFDHDDIIGWTRREGSS 451
 DB 361 OGYSVFEYGDYVGLPTHGVPMSKSIDPLQARQTYAAGTODYFDHDDIIGWTRREGSS 420
 QY 452 HPNSGLATIMSDGPGNKMVYVGGKAKGQVWRDITGNRSQVTITNADGNGFTVNGAVS 511
 DB 421 HPNSGLATIMSDGPGNKMVYVGGKAKGQVWRDITGNRSQVTITNADGNGFTVNGAVS 480
 QY 512 VVWKQ 516
 DB 481 VVWKQ 485

XX	AA070391 standard; protein; 485 AA.
ID	AA070391
XX	AA070391;
AC	
XX	
DT	16-JUL-1999 (first entry)
DE	
XX	Wild type Termamyl (RTM)-like alpha-amylase protein #7.
KW	Variant; Termamyl; alpha-amylase; mutation; Bacillus; detergent;
RW	dishwashing; laundry; textile; desizing; starch liquefaction; sweetener;
XX	ethanol.
OS	Bacillus sp.
XX	
PN	MO9919467-AI.
PD	
XX	22-APR-1999.
PF	
XX	13-OCT-1998; 98MO-DK000444.
PR	
XX	13-OCT-1997; 97DK-00001172.
PA	(NOVO) NOVO-NORDISK AS.
P1	
XX	Svendsen A, Borchert TV, Bisgard-Frantzen H;
DR	
XX	WPI; 1999-277632/23.
PT	
XX	Variant alpha-amylases - useful as detergents or for textile desizing or
PS	starch liquefaction.
XX	
XX	Disclosure; Page 72-74; 93pp; English.
CC	This sequence represents the parent sequence for new variants of a parent
CC	Termamyl-like alpha-amylase with alpha-amylase activity. The variants
CC	comprise mutations in 2-6 regions/positions relative to an alpha-amylase
CC	from either of two Bacillus species in W09526397, B. stearothermophilus,
CC	B. licheniformis, B. amyloliquefaciens or Bacillus sp. #707. The alpha-
CC	amylase variants are detergent additives for use in detergents for
CC	dishwashing, manual or automatic laundry. The variants can also be used
CC	for textile desizing or starch liquefaction (e.g. for production of
CC	sweeteners or ethanol)
XX	
SQ	Sequence 485 AA;
Query Match	91.3%; Score 2613; DB 2; Length 485;
Best Local Similarity	95.1%; Pred. No. 1.9e-205;
Matches 461; Conservative	16; Mismatches 8; Indels 0; Gaps 0;
QY	32 HHNGTGTMMQYFEHMLPNDGSHNRRLRDDAANLKSKITTAWIIPPAKGTSONDVGYGA 91
DB	1 HHNGTGTMMQYFEHWYL PNDGNHMNRL RDDAANLMSKGITTAWIIPPAKGTSONDVGYGA 60
QY	92 YDLVDLGEFNQGVTRTKYGTGRSLOGAVTSLKNNGI QVYGDUVMNHKGGADGETEMNAV 151
DB	61 YDLVDLGEFNQGVTRTKYGTGRNOLAATSLKNNGIQVYGDVVNMHHKGGAGTEIVNAV 120
QY	152 EVNRSNRNOEISGEYTIEMATYKDFPPRGANTHSNEKRWYHFHDGTDMDQSROLONKIYKF 211
DB	121 EVNRSNRNOETSGEYAIEAMTKFDFPGRGNNHSSFKRMWHFDGTDMDQSROLONKIYKF 180
QY	212 RGCGKAWDEVDIDENNNYDIWMADI DMHPYINELRWGWYNNTLTALDGFRI DAYKH 271
DB	181 RGCGKAWDEVVDIDENNNDYILMAADVDMHPHYIHFLRWGWYNYNTLTALDGFRI DAYKH 240
QY	272 IKKSYRRDWLTHFRANTTGKPMFAVAEPFMKDUALAIENYLNKTSNMNSVEVDLPHLYNA 331
DB	241 IKKSPFRDWLTHFRANTTGKPMFAVAEPFMKDUALAIENYLNKTSNMNSVEVDLPHLYNA 300
QY	332 SNGSGYEDMKNLINGSVQKP IHAVTFTVDNHDSDGEGALIESVGSMFPPLAYALITRE 391

Accession	Source	Protein	Length	Weight	PI	Ref
Db	301	SNSSGYYDMRNILNGSVVQKHPTAVTVFDVNDHSDQPEALESPFOQMFKPLAVLVLRLRE	360			
Oy	392	QGYSVFVGYDYYGIPTRGVPEMSKSIDPLQARQTVAYGQHDYFDHDDITGWTREDDSS	451			
Db	361	QGYSVFVGYDYYGIPTRGVPEMSKSIDPLQARQTVAYGQHDYFDHDDITGWTREDDSS	420			
Oy	452	HPNSGLATINSDGGGKMKMYVGGKHKAGQVWRDITGNRSCTVITNAQSGMFTNNGAVS	511			
Db	421	HPNSGLATINSDGGGKMKMYVGGKHKAGQVWRDITGNRTGTVTINADGMFNFSVNGGSVS	480			
Oy	512	VWVKO 516				
Db	481	VWVKO 485				
RESULT 12						
AAV07381						
ID	AAV07381	standard; protein; 485 AA.				
XX	AAV07381;					
XX	16-JUL-1999	(first entry)				
DE	Wild type Termamyl (RTM)-like alpha-amylase protein #1.					
XX	Variant; Termamyl; alpha-amylase; mutation; Bacillus; detergent;					
KW	dishwashing; laundry; textile; desizing; starch liquefaction; sweetener;					
XX	ethanol.					
OS	Bacillus sp.					
XX						
FH	Key	Location/Qualifiers				
FT	Misc-difference	181. .184				
FT	/note= "optionally 1, 2, 3 or all residues are deleted"					
FT	Misc-difference	195				
FT	/note= "optionally altered to any amino acid except an					
FT	Asn residue"					
FT	Misc-difference	206				
FT	/note= "optionally altered to any amino acid except a Val					
FT	residue"					
FT	Misc-difference	212				
FT	/note= "optionally altered to any amino acid except a Glu					
FT	residue"					
FT	Misc-difference	216				
FT	/note= "optionally altered to any amino acid except a Glu					
FT	residue"					
FT	Misc-difference	269				
FT	/note= "optionally altered to any amino acid except a Lys					
FT	residue"					
XX						
XX	WO9919467-A1.					
XX						
XX	22-APR-1999.					
XX						
XX	13-OCT-1998;	98WO-DK000444.				
XX						
XX	13-OCT-1997;	97DK-00001172.				
XX						
XX	(NOVO) NOVO-NORDISK AS.					
XX						
XX	Svendensen A, Borchert TV, Bisgard-Frantzen H;					
XX						
XX	WPI, 1999-277632/23.					
XX						
XX	Variant alpha-amylases - useful as detergents or for textile desizing or					
XX	starch liquefaction.					
XX						
XX	Claim 1; Page 61-63; 93pp; English.					
XX						
XX	This sequence represents the parent sequence for new variants of a parent					
XX	Termamyl-like alpha-amylase with alpha-amylase activity. The variants					
XX	comprise mutations in 2-6 regions/positions relative to an alpha-amylase					
XX	from either of two Bacillus species in WO9526397, B. stearothermophilus,					

CC B. licheniformis, B. amyloliquefaciens or Bacillus sp. #707. The alpha-
CC amylase variants are detergent additives for use in detergents for
CC dishwashing, manual or automatic laundry. The variants can also be used
CC for textile desizing or starch liquefaction (e.g. for production of
CC sweeteners or ethanol)

XX Sequence 485 AA;

Query Match 91.3%; Score 2613; DB 2; Length 485;

Best Local Similarity 95.1%; Pred. No. 1.9e-205; Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

```
QY 32 HHNGTNGTMMQYFEWHLFNDGNHNRRLDDANLKSKITAVWIPPAKGTSONDVGYGA 91
DB 1 HHNGTNGTMMQYFEWHLFNDGNHNRRLDDANLKSKITAVWIPPAKGTSONDVGYGA 60
QY 92 YDLVDLGEFNQKGVTRTKYGRNQLQAAVTSLKNNGIQVYGDVVMNHKGADGTEMVNAV 151
DB 61 YDLVDLGEFNQKGVTRTKYGRNQLQAAVTSLKNNGIQVYGDVVMNHKGADGTEMVNAV 120
QY 152 EVNSNRNOEISGEYTIETAMTKFDPFGNGNTHSNFKRWYHFDGTDMDQSRQLQNKIKYKF 211
DB 121 EVNSNRNOEISGEYTIETAMTKFDPFGNGNTHSNFKRWYHFDGTDMDQSRQLQNKIKYKF 180
QY 212 RGTGKAMDMEVDIENGNDYLMYADIDMDHEVINELNMGVWYNTNTLNDGFRIDAVKH 271
DB 181 RGTGKAMDMEVDIENGNDYLMYADIDMDHEVINELNMGVWYNTNTLNDGFRIDAVKH 240
QY 272 IKYSTTRDMLTHVNTTCKPMPFAVAEFWKNDLAAIENTLNTKSNHVSFEDVPLHNLVNA 331
DB 241 IKYSTTRDMLTHVNTTCKPMPFAVAEFWKNDLAAIENTLNTKSNHVSFEDVPLHNLVNA 300
QY 332 SNSGGYFPMRNIILNGSVVQKPIHATFVDNHDSPGEGALSFVQSWFKPLAVALVLTRE 391
DB 301 SNSGGYFPMRNIILNGSVVQKPIHATFVDNHDSPGEGALSFVQSWFKPLAVALVLTRE 360
QY 392 QGYPSVFYGDYGIPTHGVPSPKSKIDPLQARQYAGTQHDYFDHDDIIGMTRREGSS 451
DB 361 QGYPSVFYGDYGIPTHGVPSPKSKIDPLQARQYAGTQHDYFDHDDIIGMTRREGSS 420
QY 452 HPNSGLATIMSDGPGNKMVYGVKHKAGQVWRDITGNRS GTVTINADMGNFYVNGAVS 511
DB 421 HPNSGLATIMSDGPGNKMVYGVKHKAGQVWRDITGNRS GTVTINADMGNFYVNGAVS 480
QY 512 VVWVKQ 516
DB 481 VVWVKQ 485
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RESULT 13

AA99602 ID AA99602 standard; protein; 485 AA.

AA99602;

04-SEP-2000 (first entry)

Bacillus parent Termamyl-like alpha-amylase #1.

Bacillus; alpha-amylase; washing; textile desizing; starch liquefaction;
KW saccharification; muten; mutant; enzyme stability; hybrid.

Bacillus sp.

MO200029560-A1.

25-MAY-2000.

16-NOV-1999; 99WO-DK000628.

16-NOV-1998; 98DK-00001495.

(NOVO) NOVO-NORDISK AS.

XX Svendsen A, Kjaerulf S, Biegard-Frantzen H, Andersen C;
PI WPI: 2000-38777/73.
XX N-PSDB; AAA48480.

Variant of parent termamyl-like alpha amylase useful for washing, textile
desizing and starch liquefaction, comprising alterations in one or more
solvent exposed amino acid residues.

Claim 8, Page 53-54; 80pp; English.

The present sequence is a parent Termamyl-like alpha-amylase from which
mutants with increased stability at acidic pH, low calcium concentration
and high temperatures have been derived. The sequence encoding this
protein was isolated from a Bacillus genomic DNA library. A variant may
contain mutations in one or more solvent exposed amino acid residues to
increase the overall hydrophobicity of the enzyme or the overall number
of methyl groups in the side chains of exposed residues may be increased.
The mutations can be incorporated by site-directed mutagenesis or by
random mutagenesis. As a result of their increased stability, the
CC variants are suitable for the industrial processing of starch, i.e.
CC starch liquefaction and saccharification. They may also be useful for
CC washing, dishwashing and textile desizing. Hybrid alpha-amylases
CC comprising partial amino acid sequences derived from two or more alpha-
CC amylases have also been created in order to increase enzyme stability

Sequence 485 AA;

Query Match 91.3%; Score 2613; DB 3; Length 485;

Best Local Similarity 95.1%; Pred. No. 1.9e-205; Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

```
QY 32 HHNGTNGTMMQYFEWHLFNDGNHNRRLDDANLKSKITAVWIPPAKGTSONDVGYGA 91
DB 1 HHNGTNGTMMQYFEWHLFNDGNHNRRLDDANLKSKITAVWIPPAKGTSONDVGYGA 60
QY 92 YDLVDLGEFNQKGVTRTKYGRNQLQAAVTSLKNNGIQVYGDVVMNHKGADGTEMVNAV 151
DB 61 YDLVDLGEFNQKGVTRTKYGRNQLQAAVTSLKNNGIQVYGDVVMNHKGADGTEMVNAV 120
QY 152 EVNSNRNOEISGEYTIETAMTKFDPFGNGNTHSNFKRWYHFDGTDMDQSRQLQNKIKYKF 211
DB 121 EVNSNRNOEISGEYTIETAMTKFDPFGNGNTHSNFKRWYHFDGTDMDQSRQLQNKIKYKF 180
QY 212 RGTGKAMDMEVDIENGNDYLMYADIDMDHEVINELNMGVWYNTNTLNDGFRIDAVKH 271
DB 181 RGTGKAMDMEVDIENGNDYLMYADIDMDHEVINELNMGVWYNTNTLNDGFRIDAVKH 240
QY 272 IKYSTTRDMLTHVNTTCKPMPFAVAEFWKNDLAAIENTLNTKSNHVSFEDVPLHNLVNA 331
DB 241 IKYSTTRDMLTHVNTTCKPMPFAVAEFWKNDLAAIENTLNTKSNHVSFEDVPLHNLVNA 300
QY 332 SNSGGYFPMRNIILNGSVVQKPIHATFVDNHDSPGEGALSFVQSWFKPLAVALVLTRE 391
DB 301 SNSGGYFPMRNIILNGSVVQKPIHATFVDNHDSPGEGALSFVQSWFKPLAVALVLTRE 360
QY 392 QGYPSVFYGDYGIPTHGVPSPKSKIDPLQARQYAGTQHDYFDHDDIIGMTRREGSS 451
DB 361 QGYPSVFYGDYGIPTHGVPSPKSKIDPLQARQYAGTQHDYFDHDDIIGMTRREGSS 420
QY 452 HPNSGLATIMSDGPGNKMVYGVKHKAGQVWRDITGNRS GTVTINADMGNFYVNGAVS 511
DB 421 HPNSGLATIMSDGPGNKMVYGVKHKAGQVWRDITGNRS GTVTINADMGNFYVNGAVS 480
QY 512 VVWVKQ 516
DB 481 VVWVKQ 485
```

RESULT 14

AA99608 ID AA99608 standard; protein; 485 AA.

XX	AAV99608;
AC	
XX	
DT	04-SEP-2000 (first entry)
DE	Bacillus Termamyl-like alpha-amylase.
XX	
KW	Bacillus; alpha-amylase; washing; textile desizing; starch liquefaction;
KM	saccharification; muten; mutant; enzyme stability; hybrid.
XX	
OS	Bacillus sp.
XX	
PN	MO200029560-A1.
PD	25-MAY-2000.
PR	16-NOV-1999; 99WO-DK000628.
XX	
XX	16-NOV-1998; 98DK-00001495.
PA	(NOVO) NOVO-NORDISK AS.
PI	Svendsen A, Kjaerulf S, Bisgard-Frantzen H, Andersen C;
XX	WPI; 2000-387777/33.
DR	
XX	
PT	Variant of parent termamyl-like alpha amylase useful for washing, textile
PT	desizing and starch liquefaction, comprising alterations in one or more
PT	solvent exposed amino acid residues.
PS	
XX	Claim 8; Page 62-64; 8opp; English.
CC	
XX	The present sequence is a parent alpha-amylase from which mutants with
CC	increased stability at acidic pH, low calcium concentration and high
CC	temperatures have been derived. The sequence encoding this enzyme was
CC	isolated from a Bacillus genomic DNA library. A variant may contain
CC	mutations in one or more solvent exposed amino acid residues to increase
CC	the overall hydrophobicity of the enzyme or the overall number of methyl
CC	groups in the side chains of exposed residues may be increased. The
CC	mutations can be incorporated by site-directed mutagenesis or by random
CC	mutagenesis. As a result of their increased stability, the variants are
CC	suitable for the industrial processing of starch, i.e. starch
CC	liquefaction and saccharification. They may also be useful for washing,
CC	dishwashing and textile desizing. Hybrid alpha-amylases comprising
CC	partial amino acid sequences derived from two or more alpha-amylases have
CC	also been created in order to increase enzyme stability
CC	
SO	Sequence 485 AA;
Query Match	91.3%; Score 2613; DB 3; Length 485;
Best Local Similarity	95.1%; Pred. No. 1.9e-205;
Matches 461; Conservative	16; Mismatches 8; Indels 0; Gaps 0;
DY	32 HHNGTGMQVFEEHLLPFDGNNHRRLRDDAANLKSGLTAVIWPAMKGTSONDVGA 91
Db	1 HHNGTGMQVFEEHLLPFDGNNHRRLRDDAANLKSGLTAVIWPAMKGTSONDVGA 60
DY	92 YDLYDLGFNQKGVRTKYGRTSLOQAVTSLKNNGIQVYGDVVMNHKGADGTEVNAY 151
Db	61 YDLYDLGFNQKGVRTKYGRTEHQQLQAATVSLKNNGIQVYGDVVMMHKGGAGTEIVNAV 120
DY	152 EVNNSNRROELSGEETITAMRKEDPPRGNGTHSKRMWRHYHGDDGDMQOSROLQNKIKFE 211
Db	121 EVNNSNRROELTSGEYAIAEMTKFDFPGKGNNSHSEFKMRWHHDGTDMDQSROLQNKIKFE 180
DY	212 RGTGKAMDWEVDIENGANYDYIMYADIDMDHPVELLNHWGWYNTNLDSFRIDA VKH 271
Db	181 RGTGKAMDWEVDTEGNNDYLIMAYADVMDHDPVEIHENRWGWYNTNLDSFRIDA VKH 240
DY	272 IKISTRTDMLTHVRNTTGKPMFAVAEFMKNDLAIENTLAKTSQASHASFDVDLHNLYNA 331
Db	241 IKISTRTDMLTHVRNTTGKPMFAVAEFMKNDLGAIENTLAKTSQASHASFDVDLHNLYNA 300

Qy	332	SNNGGFEDMRNLINSVQKPHIAVTVDMHDSQPGALSESFQSWFKELAALITRE	391
Db	301	SNNGGYDMRNLINSVQKPHIAVTVDMHDSQPGALSESFVQWFKELAALVITRE	360
Qy	392	QGYPSVFYGDYYGIFPHGVPSMKSXKIDPLLQARQTYAYGCHDFPDHDDITGMTREDS	451
Db	361	QGYPSVFYGDYYGIFPHGVPAKSKSIDPLLQARQTFALGCHDFPDHDDITGMTRECNSS	420
Qy	452	HPNSGLATIMSDGPGGNKMVYGGKKAKQVWRDITGRNSGVTILNADGMNFTVNGAVS	511
Db	421	HPNSGLATIMSDGPGGNKMVYGGKKAKQVWRDITGRNRTGTITLNAQGMNFTVNGSSVS	480
Qy	512	VWVKQ 516	
Db	481	VWVKQ 485	
RESULT 15			
AB069933	ID	ABB06933 standard; protein; 485 AA.	
AC	XX	ABB06933;	
DT	XX	19-JUN-2002 (first entry)	
XX	DE	Bacillus termamyl-like alpha-amylase protein SEQ ID NO:2.	
KW	XX	Bacillus; 'termamyl'-like alpha-amylase; alpha-amylase; EC 3.2.1.1;	
KM	XX	variant; mutant; enzyme; protein co-ordinate data; cleaning; detergent;	
KM	XX	washing; sweetener; ethanol; starch.	
OS	XX	Bacillus sp.	
XX	XX	WC0200166712-A2.	
XX	XX	13-SEP-2001.	
PF	XX	07-MAR-2001; 2001WO-DK000144.	
XX	XX	08-MAR-2000; 2000DK-00000376.	
PR	XX	15-MAR-2000; 2000US-0189857P.	
PR	XX	23-FEB-2001; 2001DK-00000303.	
PR	XX	26-FEB-2001; 2001US-0271382P.	
XX	XX	(NOVO) NOVONZYMES AS.	
XX	XX	Andersen C, Borchert TV, Nielsen BR;	
XX	XX	WPI; 2002-239612/29.	
XX	XX	N-PSDB; ABL50564.	
PT	XX	Novel variant of parent termamyl-like alpha-amylase useful as a component	
PT	XX	in washing and dishwashing compositions, for textile desizing, for starch	
XX	XX	liquefaction, and for producing sweeteners and ethanol from starch.	
PS	XX	Claim 8; Page 132-133; 153pp; English.	
XX	XX	The present invention describes a variant of a parent termamyl-like alpha	
CC	XX	-amylase (EC 3.2.1.1) (1) comprising an alteration at one or more	
CC	XX	positions of a group of 31 possible amino acid positions. The alteration	
CC	XX	in (1) may be at Arg28, Arg118, Asn174, Arg181, Gly182, Asp183, Gly184,	
CC	XX	Gly186, Trp189, Asn195, Met202, Tyr298, Asn299, Lys303, Asn306,	
CC	XX	Arg310, Asn314, Arg330, His324, Glu345, Tyr396, Arg400, Trp439, Arg444,	
CC	XX	Asn445, Lys446, Glu449, Arg458, Asn471, or Asn484. (1) can be used for	
CC	XX	washing and/or dishwashing, textile desizing, and starch liquefaction.	
CC	XX	(1) is useful as a component in hard surface cleaning detergent	
CC	XX	composition, and for producing sweeteners and ethanol from starch. (1)	
CC	XX	has altered solubility, preferably increased solubility, in particular	
CC	XX	under washing, dish washing or hard surface cleaning conditions. The	
CC	XX	present sequence represents a Bacillus termamyl-like alpha-amylase which	
CC	XX	is used in the exemplification of the present invention	
Qy	Sequence 485 AA;		

Query Match 91.3%; Score 2613; DB 5; Length 485;
 Best Local Similarity 95.1%; Pred. No. 1.9e-205;
 Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

Qy	32	HHNGTNGTMOYFEWHLNDGNHNRRLDDAANKSGITAWIIPPAWKGSQNDVGGA	91
Db	1	HHNGTNGTMOYFEWHLNDGNHNRRLDDAANKSGITAWIIPPAWKGSQNDVGGA	60
Qy	92	YDLVDLGEFNKGTVRTKYSRQLOGAVSLKNNGLIOVGDVNNHKGADGTEMNAV	151
Db	61	YDLVDLGEFNKGTVRTKYSRQLOGAVSLKNNGLIOVGDVNNHKGADGTEIYNAV	120
Qy	152	EVNSNRNQEISGEYTIEMTKFDEPGRGNTHSNFKRMYPDGTMDQSRLOQNKIYKF	211
Db	121	EVNSNRNQEISGEYTIEMTKFDEPGRGNTHSNFKRMYPDGTMDQSRLOQNKIYKF	180
Qy	212	RGTGKAMDWEVDIENGNDYLMYADIDMDHPEVINELRNMGWYNTNTLNLGFRIDAVKH	271
Db	181	RGTGKAMDWEVDIENGNDYLMYADIDMDHPEVINELRNMGWYNTNTLNLGFRIDAVKH	240
Qy	272	IKYESTRDMULTHVNTTGGKMPAFAEFWKNDLAIENYLNKTSWNHVSFDVPLHYNLYNA	331
Db	241	IKYESTRDMULTHVNTTGGKMPAFAEFWKNDLAIENYLNKTSWNHVSFDVPLHYNLYNA	300
Qy	332	SNSGAYFDMRNILNGSVYQKPIHAVTFVDNHDSDQGEALBSFVQSWFKPLAYALLTRE	391
Db	301	SNSGAYFDMRNILNGSVYQKPIHAVTFVDNHDSDQGEALBSFVQSWFKPLAYALLTRE	360
Qy	392	QGYPSVFYGDYGGIPTHGVPMSKSIDPLQARQTYAYGTQHDYFDHDIIGMTREGDSS	451
Db	361	QGYPSVFYGDYGGIPTHGVPMSKSIDPLQARQTYAYGTQHDYFDHDIIGMTREGDSS	420
Qy	452	HPNSGLATIMSDGPGNKMVYVGGKAGQVWRDITGNRSSTVTINADGKGFYNGGAVS	511
Db	421	HPNSGLATIMSDGPGNKMVYVGGKAGQVWRDITGNRSSTVTINADGKGFYNGGAVS	480
Qy	512	VMVKQ 516	
Db	481	VMVKQ 485	

Search completed: May 2, 2005, 21:54:47
 Job time : 80 secs

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OM protein - protein search, using sw model

Run on: May 2, 2005, 21:41:18 ; Search time 24 Seconds
(without alignments)
1604.955 Million cell updates/sec

Title: US-08-952-741-2
2862
Perfect score: 1 MKLHNRILSVLTLLAVAV.....ADGWGNFTVNGAVSVWVKQ 516
Sequence:

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/PTCUTS_COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2862	100.0	516	US-09-986-676A-2	Sequence 2, Appli
2	2862	100.0	516	US-09-971-611-2	Sequence 2, Appli
3	2713	94.8	485	US-09-291-023A-18	Sequence 18, Appli
4	2713	94.8	485	US-09-381-687-1	Sequence 1, Appli
5	2713	94.8	485	US-09-340-715A-18	Sequence 18, Appli
6	2613	91.3	485	US-08-446-803-1	Sequence 1, Appli
7	2613	91.3	485	US-08-861-837-1	Sequence 1, Appli
8	2613	91.3	485	US-08-600-908A-12	Sequence 12, Appli
9	2613	91.3	485	US-08-683-838A-12	Sequence 12, Appli
10	2613	91.3	485	US-08-600-656-1	Sequence 1, Appli
11	2613	91.3	485	US-09-170-670-1	Sequence 1, Appli
12	2613	91.3	485	US-09-170-670-7	Sequence 1, Appli
13	2613	91.3	485	US-09-193-068-1	Sequence 1, Appli
14	2613	91.3	485	US-09-193-068-7	Sequence 7, Appli
15	2613	91.3	485	US-09-183-412-1	Sequence 1, Appli
16	2613	91.3	485	US-09-183-412-7	Sequence 7, Appli
17	2613	91.3	485	US-09-354-191A-1	Sequence 1, Appli
18	2613	91.3	485	US-09-291-023A-19	Sequence 19, Appli
19	2613	91.3	485	US-09-290-734-1	Sequence 1, Appli
20	2613	91.3	485	US-09-290-734-7	Sequence 7, Appli
21	2613	91.3	485	US-09-636-252A-12	Sequence 12, Appli
22	2613	91.3	485	US-09-381-687-2	Sequence 2, Appli
23	2613	91.3	485	US-09-545-586-1	Sequence 1, Appli
24	2613	91.3	485	US-09-545-586-7	Sequence 7, Appli
25	2613	91.3	485	US-09-540-715A-19	Sequence 19, Appli
26	2613	91.3	485	US-09-769-864-1	Sequence 1, Appli
27	2613	91.3	485	US-09-769-864-7	Sequence 7, Appli

28	2609	91.2	485	3	US-09-264-097-7	Sequence 7, Appli
29	2598.5	90.8	486	4	US-09-381-687-4	Sequence 4, Appli
30	2440	85.3	485	2	US-08-446-803-2	Sequence 2, Appli
31	2440	85.3	485	2	US-08-861-837-2	Sequence 2, Appli
32	2440	85.3	485	3	US-08-600-656-2	Sequence 2, Appli
33	2440	85.3	485	3	US-09-170-670-2	Sequence 2, Appli
34	2440	85.3	485	3	US-09-170-670-8	Sequence 8, Appli
35	2440	85.3	485	3	US-09-193-068-2	Sequence 2, Appli
36	2440	85.3	485	3	US-09-193-068-8	Sequence 8, Appli
37	2440	85.3	485	3	US-09-183-412-2	Sequence 2, Appli
38	2440	85.3	485	3	US-09-183-412-8	Sequence 8, Appli
39	2440	85.3	485	3	US-09-264-097-5	Sequence 5, Appli
40	2440	85.3	485	3	US-09-354-191A-2	Sequence 2, Appli
41	2440	85.3	485	3	US-09-290-734-2	Sequence 2, Appli
42	2440	85.3	485	3	US-09-290-734-8	Sequence 8, Appli
43	2440	85.3	485	4	US-09-381-687-3	Sequence 3, Appli
44	2440	85.3	485	4	US-09-545-586-2	Sequence 2, Appli
45	2440	85.3	485	4	US-09-545-586-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-986-676A-2
Sequence 2, Application US/09986676A
Patent No. 6638748
GENERAL INFORMATION:
APPLICANT: HATADA, Yuji
APPLICANT: OZAKI, Katsuya
APPLICANT: ARA, Katsutoshi
APPLICANT: KAWAI, Shuji
APPLICANT: ITO, Susumu
TITLE OF INVENTION: Gene Encoding Alkaline Liquefying Alpha-Amylase
FILE REFERENCE: 2173-0121P
CURRENT APPLICATION NUMBER: US/09/986, 676A
CURRENT FILING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: PCT/JP96/01641
PRIOR FILING DATE: 1996-06-14
PRIOR APPLICATION NUMBER: Japan 147257/1995
PRIOR FILING DATE: 1995-06-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 2
LENGTH: 516
TYPE: PRT
ORGANISM: Bacillus sp.
US-09-986-676A-2

Query Match 100.0%; Score 2862; DB 4; Length 516;
Best Local Similarity 100.0%; Pred. No. 1.1e-250;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MKLHNRILSVLTLLAVAVLPYMTBPAQHNGTGMQYFEHMLPNDGNHNRIRD	60
DB	1	MKLHNRILSVLTLLAVAVLPYMTBPAQHNGTGMQYFEHMLPNDGNHNRIRD	60
QY	61	DAANLKSQGITAVWIPPAWPGTSONDVGYGAYDLYDGEFNQGTVAATKGTSSQLOGAV	120
DB	61	DAANLKSQGITAVWIPPAWPGTSONDVGYGAYDLYDGEFNQGTVAATKGTSSQLOGAV	120
QY	121	TSLKNGGIQYGGVVMNHKGGADGTEKVNAVEVRSNRNOISGEYTIEMTKDFPGRG	180
DB	121	TSLKNGGIQYGGVVMNHKGGADGTEKVNAVEVRSNRNOISGEYTIEMTKDFPGRG	180
QY	181	NTSNFPMRYHFDGDMDSROLQNKTYFRGKAWDEVDIENGNYLYIWAADIDMD	240
DB	181	NTSNFPMRYHFDGDMDSROLQNKTYFRGKAWDEVDIENGNYLYIWAADIDMD	240
QY	241	HPEVINELRWGQWYNTNLNDGFRIDAVGHIKYSTYRDLTHVRNTTGKMPFAVAEFWK	300
DB	241	HPEVINELRWGQWYNTNLNDGFRIDAVGHIKYSTYRDLTHVRNTTGKMPFAVAEFWK	300

QY 301 NDAALENTKNTSMNHSVDFVPLHYNLYNASNGGFEDMRNTLNSVVOGKPIHATVTV 360
DB 301 NDAALENTKNTSMNHSVDFVPLHYNLYNASNGGFEDMRNTLNSVVOGKPIHATVTV 360
QY 361 DNHDSPGALLESFVQSWFKPLAYALILTRREGQPSVFGDYGIPTHGVPMSKSIDPL 420
DB 361 DNHDSPGALLESFVQSWFKPLAYALILTRREGQPSVFGDYGIPTHGVPMSKSIDPL 420
QY 421 LQARQTYAGTGDHDFDHDHDIIGWTREGDSHPNSGLATIMSDPGGNKMYVGKHKACQ 480
DB 421 LQARQTYAGTGDHDFDHDHDIIGWTREGDSHPNSGLATIMSDPGGNKMYVGKHKACQ 480
QY 481 VWRDITGNRSCTVTINADGNGFTVNGGAVSVWVWQ 516
DB 481 VWRDITGNRSCTVTINADGNGFTVNGGAVSVWVWQ 516

RESULT 2
US-09-971-611-2
Sequence 2, Application US/09971611
Patent No. 6743616
GENERAL INFORMATION:
APPLICANT: ARAKI, HIROYUKI
APPLICANT: ENDO, KEIJI
APPLICANT: HACHIMARA, HIROSHI
APPLICANT: IGARASHI, KAZUAKI
APPLICANT: HAYASHI, YASUHIRO
APPLICANT: OZAKI, KATSUYA
TITLE OF INVENTION: HIGHLY PRODUCTIVE ALPHA-AMYLASES
FILE REFERENCE: 214377US0
CURRENT APPLICATION NUMBER: US/09/971, 611
CURRENT FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: JP 2000/310605
PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 516
TYPE: PRT
ORGANISM: Bacillus sp. KSM-AP1378
US-09-971-611-2

Query Match 100.0%; Score 2862; DB 4; Length 516;

Best Local Similarity 100.0%; Pred. No. 1.1e-250; Indels 0; Gaps 0;

Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCLNRIISVLTLLLAVALFPYMTPEPAQAHNGTGMQYFEMHLPNDGNHNRRLRD 60
DB 1 MCLNRIISVLTLLLAVALFPYMTPEPAQAHNGTGMQYFEMHLPNDGNHNRRLRD 60
QY 61 DAANLSKGIITAWIPPAWKGTSQNDVGYGAYDLYDGEFNQKGTATKGTSSQOGAV 120
DB 61 DAANLSKGIITAWIPPAWKGTSQNDVGYGAYDLYDGEFNQKGTATKGTSSQOGAV 120
QY 121 TSJKNNGIOYGVGVNMHKGADGTEWNAVEVNRSRNOEISGEYTIEMTFEDFPGRG 180
DB 121 TSJKNNGIOYGVGVNMHKGADGTEWNAVEVNRSRNOEISGEYTIEMTFEDFPGRG 180
QY 181 NTHSNFMRWYHFDGTDMDQSRQONKIYKFRGTGKADWEVDIENGNYDYLWYADIDMD 240
DB 181 NTHSNFMRWYHFDGTDMDQSRQONKIYKFRGTGKADWEVDIENGNYDYLWYADIDMD 240
QY 241 HPEVINELRWGWYNTLNLDFRIDAVGHIKSYSTRDWLTHVRNTTGKPMFAVAEFWK 300
DB 241 HPEVINELRWGWYNTLNLDFRIDAVGHIKSYSTRDWLTHVRNTTGKPMFAVAEFWK 300
QY 301 NDAALENTKNTSMNHSVDFVPLHYNLYNASNGGFEDMRNTLNSVVOGKPIHATVTV 360
DB 301 NDAALENTKNTSMNHSVDFVPLHYNLYNASNGGFEDMRNTLNSVVOGKPIHATVTV 360
QY 361 DNHDSPGALLESFVQSWFKPLAYALILTRREGQPSVFGDYGIPTHGVPMSKSIDPL 420
DB 361 DNHDSPGALLESFVQSWFKPLAYALILTRREGQPSVFGDYGIPTHGVPMSKSIDPL 420

QY 421 LQARQTYAGTGDHDFDHDHDIIGWTREGDSHPNSGLATIMSDPGGNKMYVGKHKACQ 480
DB 421 LQARQTYAGTGDHDFDHDHDIIGWTREGDSHPNSGLATIMSDPGGNKMYVGKHKACQ 480
QY 481 VWRDITGNRSCTVTINADGNGFTVNGGAVSVWVWQ 516
DB 481 VWRDITGNRSCTVTINADGNGFTVNGGAVSVWVWQ 516

RESULT 3
US-09-291-023A-18

Sequence 18, Application US/09291023A

Patent No. 630871

GENERAL INFORMATION:

APPLICANT: Outtrup, Helle

APPLICANT: Borchert, Torben

APPLICANT: Nielsen, Bjarne

APPLICANT: Nielsen, Vibeke

APPLICANT: Hoeck, Lisbeth

TITLE OF INVENTION: Polypeptides Having Alkaline Alpha-amylose Activity And Nucleic Ac

FILE REFERENCE: 5821.010-US

CURRENT APPLICATION NUMBER: US/09/291,023A

CURRENT FILING DATE: 1999-04-13

PRIOR APPLICATION NUMBER: DK 1999 00438

PRIOR FILING DATE: 1999-03-31

NUMBER OF SEQ ID NOS: 21

SOFTWARE: Patentin version 3.0

SEQ ID NO 18

LENGTH: 485

TYPE: PRT

ORGANISM: Bacillus

US-09-291-023A-18

Query Match 94.8%; Score 2713; DB 3; Length 485;

Best Local Similarity 100.0%; Pred. No. 3.2e-237; Indels 0; Gaps 0;

Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 HNGTNGTGMQYFEMHLPNDGNHNRRLRDANLSKGIITAWIPPAWKGTSQNDVGYG 91
DB 1 HNGTNGTGMQYFEMHLPNDGNHNRRLRDANLSKGIITAWIPPAWKGTSQNDVGYG 60
QY 92 YDLYDGEFNQKGTATKGTSSQOGAVTSJKNNGIOYGVGVNMHKGADGTEWNAV 151
DB 92 YDLYDGEFNQKGTATKGTSSQOGAVTSJKNNGIOYGVGVNMHKGADGTEWNAV 120
QY 152 EVNRSNRNOEISGEYTIEMTFEDFPGRGNTSHNFWYHFDGTDMDQSRQONKIYK 211
DB 152 EVNRSNRNOEISGEYTIEMTFEDFPGRGNTSHNFWYHFDGTDMDQSRQONKIYK 180
QY 212 RGTGKADWEVDIENGNYDYLWYADIDMDHPEVINELRWGWYNTLNLDFRIDAVGH 271
DB 212 RGTGKADWEVDIENGNYDYLWYADIDMDHPEVINELRWGWYNTLNLDFRIDAVGH 240
QY 272 IKSYSTRDWLTHVRNTTGKPMFAVAEFWKNDLAAIENYLNKNTSMNHSVDFVPLHYNLYNA 331
DB 272 IKSYSTRDWLTHVRNTTGKPMFAVAEFWKNDLAAIENYLNKNTSMNHSVDFVPLHYNLYNA 300
QY 332 SNSGGYFEDMRNTLNSVVOGKPIHATVFDVNDHSDPGALLESFVQSWFKPLAYALILTR 391
DB 332 SNSGGYFEDMRNTLNSVVOGKPIHATVFDVNDHSDPGALLESFVQSWFKPLAYALILTR 360
QY 392 QGYPSVFGDYGIPTHGVPMSKSIDPLQARQTYAGTGDHDFDHDHDIIGWTREGDS 451
DB 392 QGYPSVFGDYGIPTHGVPMSKSIDPLQARQTYAGTGDHDFDHDHDIIGWTREGDS 420
QY 452 HPSGALTIMSDPGGNKMYVGKHKAGOVWRDITGNRSCTVTINADGNGFTVNGGAVS 511
DB 452 HPSGALTIMSDPGGNKMYVGKHKAGOVWRDITGNRSCTVTINADGNGFTVNGGAVS 480
QY 512 VWVWQ 516
DB 512 VWVWQ 516

Db 481 VVWQ 485

RESULT 4
US-09-381-687-1
; Sequence 1, Application US/09381687
; Patent No. 6486113
; GENERAL INFORMATION:
; APPLICANT: HATADA, Yoji
; APPLICANT: IKAWA, Kaori
; APPLICANT: ITO, Susumu
; APPLICANT: IGARASHI, Kazuaki
; APPLICANT: HAGIHARA, Hiroshi
; APPLICANT: HAYASHI, Yasuhiro
; APPLICANT: ARAKI, Hiroyuki
; APPLICANT: OZAKI, Katsuya
; TITLE OF INVENTION: MUTANT ALPHA-AMYLASES
; FILE REFERENCE: 2173-0115P
; CURRENT APPLICATION NUMBER: US/09/381,687
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp. KSM-AP 1378
US-09-381-687-1

Query Match 94.8%; Score 2713; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 3.2e-237;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 HHNGTNGTMMQYFEFHL.PNDGNHNRRLRDDAANKSKGITAVWLP.PAMKGSQNDVGYGA 91
Db 1 HHNGTNGTMMQYFEFHL.PNDGNHNRRLRDDAANKSKGITAVWLP.PAMKGSQNDVGYGA 60

Qy 92 YDLVDLGEFNQKGTVRKTYGTRSQLQGAVTSLKNGNGIOVGDVVMNHKGADGTEMNAV 151
Db 61 YDLVDLGEFNQKGTVRKTYGTRSQLQGAVTSLKNGNGIOVGDVVMNHKGADGTEMNAV 120

Qy 152 EVNRSNNOEISGEYITEAMTKFDPGKGNTHSNFKRWYHFDGTDMDQSRQLOKNIYKF 211
Db 121 EVNRSNNOEISGEYITEAMTKFDPGKGNTHSNFKRWYHFDGTDMDQSRQLOKNIYKF 180

Qy 212 RGCGKAMDWEVDLNGNVDYLMYADIMDHPEVINELRNMGWYTNLTLDGFRIDAVKH 271
Db 181 RGCGKAMDWEVDLNGNVDYLMYADIMDHPEVINELRNMGWYTNLTLDGFRIDAVKH 240

Qy 272 IKYSYTRDMLTHVANTGKPMFAVAEFKNDLAIENYLNKTSNHSVFDVPLHYNLNA 331
Db 241 IKYSYTRDMLTHVANTGKPMFAVAEFKNDLAIENYLNKTSNHSVFDVPLHYNLNA 300

Qy 332 SNSGGEFDMENILNGSVVQKHPHIAVTFVNDHDSQPEGALESFVQSWFKPLAYALLITRE 391
Db 301 SNSGGEFDMENILNGSVVQKHPHIAVTFVNDHDSQPEGALESFVQSWFKPLAYALLITRE 360

Qy 392 QGYPSVFGDYGGI.PTHGVPSMSKIDPLLOAQRTYAVGTOHDYFDHDDIIGWTRREGDSS 451
Db 361 QGYPSVFGDYGGI.PTHGVPSMSKIDPLLOAQRTYAVGTOHDYFDHDDIIGWTRREGDSS 420

Qy 452 HPNSGLATTMSDGGKMKMYVVGKKGAVWRDITGRSGTIVTINADGKGNFTVNGGAVS 511
Db 421 HPNSGLATTMSDGGKMKMYVVGKKGAVWRDITGRSGTIVTINADGKGNFTVNGGAVS 480

Qy 512 VVWQ 516
Db 481 VVWQ 485

RESULT 5
US-09-540-715A-18
; Sequence 18, Application US/09540715A
; Patent No. 6623348

; GENERAL INFORMATION:
; APPLICANT: Outterup, Helle
; APPLICANT: Borchert, Torben
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nielsen, Vibeke
; APPLICANT: Hoeck, Lisbeth
; TITLE OF INVENTION: Polypeptides Having Alkaline Alpha-amyase Activity And Nucleic A
; FILE REFERENCE: 5821.010-US
; CURRENT APPLICATION NUMBER: US/09/540,715A
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/291,023
; PRIOR FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 18
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus
US-09-540-715A-18

Query Match 94.8%; Score 2713; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 3.2e-237;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 HHNGTNGTMMQYFEFHL.PNDGNHNRRLRDDAANKSKGITAVWLP.PAMKGSQNDVGYGA 91
Db 1 HHNGTNGTMMQYFEFHL.PNDGNHNRRLRDDAANKSKGITAVWLP.PAMKGSQNDVGYGA 60

Qy 92 YDLVDLGEFNQKGTVRKTYGTRSQLQGAVTSLKNGNGIOVGDVVMNHKGADGTEMNAV 151
Db 61 YDLVDLGEFNQKGTVRKTYGTRSQLQGAVTSLKNGNGIOVGDVVMNHKGADGTEMNAV 120

Qy 152 EVNRSNNOEISGEYITEAMTKFDPGKGNTHSNFKRWYHFDGTDMDQSRQLOKNIYKF 211
Db 121 EVNRSNNOEISGEYITEAMTKFDPGKGNTHSNFKRWYHFDGTDMDQSRQLOKNIYKF 180

Qy 212 RGCGKAMDWEVDLNGNVDYLMYADIMDHPEVINELRNMGWYTNLTLDGFRIDAVKH 271
Db 181 RGCGKAMDWEVDLNGNVDYLMYADIMDHPEVINELRNMGWYTNLTLDGFRIDAVKH 240

Qy 272 IKYSYTRDMLTHVANTGKPMFAVAEFKNDLAIENYLNKTSNHSVFDVPLHYNLNA 331
Db 241 IKYSYTRDMLTHVANTGKPMFAVAEFKNDLAIENYLNKTSNHSVFDVPLHYNLNA 300

Qy 332 SNSGGEFDMENILNGSVVQKHPHIAVTFVNDHDSQPEGALESFVQSWFKPLAYALLITRE 391
Db 301 SNSGGEFDMENILNGSVVQKHPHIAVTFVNDHDSQPEGALESFVQSWFKPLAYALLITRE 360

Qy 392 QGYPSVFGDYGGI.PTHGVPSMSKIDPLLOAQRTYAVGTOHDYFDHDDIIGWTRREGDSS 451
Db 361 QGYPSVFGDYGGI.PTHGVPSMSKIDPLLOAQRTYAVGTOHDYFDHDDIIGWTRREGDSS 420

Qy 452 HPNSGLATTMSDGGKMKMYVVGKKGAVWRDITGRSGTIVTINADGKGNFTVNGGAVS 511
Db 421 HPNSGLATTMSDGGKMKMYVVGKKGAVWRDITGRSGTIVTINADGKGNFTVNGGAVS 480

Qy 512 VVWQ 516
Db 481 VVWQ 485

RESULT 6
US-08-446-803-1
; Sequence 1, Application US/08446803
; Patent No. 5824531
; GENERAL INFORMATION:
; APPLICANT: Outterup, Helle
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Ostergaard, Peter Rahbek
; APPLICANT: Rasmussen, Michael Dolberg
; APPLICANT: Van Der Zee, Pia
; TITLE OF INVENTION: Alkaline Bacillus Amylase

NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: No. 58245310 No. 5824531disk of No. 5824531ch America
STREET: 405 Lexington Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446, 803
FILING DATE: 01-June-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 4157,204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 867-0123
TELEFAX: (212) 878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-446-803-1

Query Match 91.3%; Score 2613; DB 2; Length 485;
Best Local Similarity 95.1%; Pred. No. 3.7e-228;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;
QY 32 HHNGTGMQYFEWHL PNDGNHNR LRDAA NLKSKGITAWIIPAMKGTSONDVGYGA 91
DB 1 HHNGTGMQYFEWHL PNDGNHNR LRDAA NLKSKGITAWIIPAMKGTSONDVGYGA 60
QY 92 YDLYDGEFNQKGTATKXGTRSLQGA VTS LKNNGIQYVGDVVMNHKGGADGTEWNAV 151
DB 61 YDLYDGEFNQKGTATKXGTRSLQGA VTS LKNNGIQYVGDVVMNHKGGADGTEWNAV 120
QY 152 EVNRSNRNOEISGEYTI EAATKFD PFGKGNTHSFKRWYHFDGTDWDSROLQNKIYK 211
DB 121 EVNRSNRNOEISGEYTI EAATKFD PFGKGNTHSFKRWYHFDGTDWDSROLQNKIYK 180
QY 212 RGTGKAMDWEVDIENGNYDYLMTADIDMDHPEVINE LRWGWYTTNLMDGFRIDA VYK 271
DB 181 RGTGKAMDWEVDIENGNYDYLMTADIDMDHPEVINE LRWGWYTTNLMDGFRIDA VYK 240
QY 272 IKTSYTRDMLTHVRNTTGKEMPAVAEFWKNDLAIENYLNKTSWNHVSFDPPLHYLNYA 331
DB 241 IKTSYTRDMLTHVRNTTGKEMPAVAEFWKNDLAIENYLNKTSWNHVSFDPPLHYLNYA 300
QY 332 SNGGTFYDMENILNGSVYQKHPHIAVT FVDNHD SQCEAL ESTVQSKFLAYALITRE 391
DB 301 SNGGTFYDMENILNGSVYQKHPHIAVT FVDNHD SQCEAL ESTVQSKFLAYALITRE 360
QY 392 OGPAVFYGGYGIPIPHGVPSMKSIDILLQARQTA VYGTQHDYFPHHDIIGWTRBGDS 451
DB 361 OGPAVFYGGYGIPIPHGVPSMKSIDILLQARQTA VYGTQHDYFPHHDIIGWTRBGDS 420
QY 452 HPSGLATTIMSDPGGNKMYVGNKAKAGVYARDITGNRS GTVTINADGNGFTVNGAVS 511
DB 421 HPSGLATTIMSDPGGNKMYVGNKAKAGVYARDITGNRS GTVTINADGNGFTVNGAVS 480
QY 512 VVTKQ 516
DB 481 VVTKQ 485

RESULT 7
US-08-861-837-1
Sequence 1, Application US/08861837
Patent No. 5856164
GENERAL INFORMATION:
APPLICANT: Octrup, Helle
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Ostergaard, Peter Rahbek
APPLICANT: Rasmussen, Michael Dolberg
APPLICANT: Van der Zee, Pia
TITLE OF INVENTION: Alkaline Bacillus Amylase
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: No. 58561640 No. 5856164disk of No. 5856164ch America
STREET: 405 Lexington Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/861, 837
FILING DATE: 01-June-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446, 803
FILING DATE: 01-June-1995
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 4157,204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 867-0123
TELEFAX: (212) 878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-861-837-1

Query Match 91.3%; Score 2613; DB 2; Length 485;
Best Local Similarity 95.1%; Pred. No. 3.7e-228;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;
QY 32 HHNGTGMQYFEWHL PNDGNHNR LRDAA NLKSKGITAWIIPAMKGTSONDVGYGA 91
DB 1 HHNGTGMQYFEWHL PNDGNHNR LRDAA NLKSKGITAWIIPAMKGTSONDVGYGA 60
QY 92 YDLYDGEFNQKGTATKXGTRSLQGA VTS LKNNGIQYVGDVVMNHKGGADGTEWNAV 151
DB 61 YDLYDGEFNQKGTATKXGTRSLQGA VTS LKNNGIQYVGDVVMNHKGGADGTEWNAV 120
QY 152 EVNRSNRNOEISGEYTI EAATKFD PFGKGNTHSFKRWYHFDGTDWDSROLQNKIYK 211
DB 121 EVNRSNRNOEISGEYTI EAATKFD PFGKGNTHSFKRWYHFDGTDWDSROLQNKIYK 180
QY 212 RGTGKAMDWEVDIENGNYDYLMTADIDMDHPEVINE LRWGWYTTNLMDGFRIDA VYK 271
DB 181 RGTGKAMDWEVDIENGNYDYLMTADIDMDHPEVINE LRWGWYTTNLMDGFRIDA VYK 240
QY 272 IKTSYTRDMLTHVRNTTGKEMPAVAEFWKNDLAIENYLNKTSWNHVSFDPPLHYLNYA 331
DB 241 IKTSYTRDMLTHVRNTTGKEMPAVAEFWKNDLAIENYLNKTSWNHVSFDPPLHYLNYA 300
QY 332 SNGGTFYDMENILNGSVYQKHPHIAVT FVDNHD SQCEAL ESTVQSKFLAYALITRE 391

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Db      301  SMSGGYDMRNLINSVVOXKPTHTAVTFVDNHDSDGGEALIESVVOQMFPLAYALVITRE 360
Qy      392  QGPEPVFGDYDYGIEPTHGVSNMKSXIDPLLOARQTYAGTODHDFDHHDIIIGTREGDSS 451
Db      361  QGPEPVFGDYDYGIEPTHGVSNMKSXIDPLLOARQTYAGTODHDFDHHDIIIGTREGDSS 420
Qy      452  HPSGLATIMSDPGGKNKMVYVYKHKAGOVWMDITGNSGTVTINADGMGNFVNGGAVS 511
Db      421  HPSGLATIMSDPGGKNKMVYVYKHKAGOVWMDITGNTGTVTINADGMGNFVNGGAVS 480
Qy      512  VWVVKQ 516
Db      481  VWVVKQ 485

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RESULT 8

```

: Sequence 12 Application US/06600908A
: Patent No. 5989169
: GENERAL INFORMATION:
: APPLICANT: Svendsen, Allan
: APPLICANT: Bisg rd-Frantzen, Henrik
: APPLICANT: Borchert, Torben Vedel
: TITLE OF INVENTION: ``Amylase Mutants
: NUMBER OF SEQUENCES: 13
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: No. 59891690 No. 5989169disk of No. 5989169th America, Inc.
: STREET: 405 Lexington Avenue, 64th Floor
: CITY: New York
: STATE: New York
: COUNTRY: United States of America
: ZIP: 10174-6401
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/600,908A
: FILING DATE: 13-FEB-1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Green, Reza
: REGISTRATION NUMBER: 38,475
: REFERENCE/DOCKET NUMBER: 4394.204-US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-867-0123
: TELEFAX: 212-878-9655
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 485 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
:
: US-08-600-908A-12

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Query Match	91.3%	Score 2613	DB 2	Length 485
Best Local Similarity	95.1%	Pred. No. 3.7e-229		
Matches 461	Conservative 16	Mismatches 8	Indels 0	Gaps 0
QY	32	HHNGTNGTMMQYFEWHLPLDNGHNHNRRLDDDAANLKSKEITAVTWIPPAWKGTSQNDVYGCA	91	
Db	1	HHNGTNGTMMQYFEWYLLPDNGHNHNRRLDDDAANLKSKEITAVTWIPPAWKGTSQNDVYGCA	60	
QY	92	YDLIDLGEFNOKGTVRTKYGTRSQLQAVTSLKNNGIOYGEDVYNNHKGADGTEMVNAV	151	
Db	61	YDLIDLGEFNOKGTVRTKYGTRNQLOAVTSLKNNGIOYGEDVYNNHKGADGTEIVNAV	120	
QY	152	EVNSNRRQELSGEVTIEAAMTKFDPDPPGAGNHSNFKMVMYHPDGDMDQSOLOQNKIKYF	211	
Db	121	EVNSNRRQELSGEVTIEAAMTKFDPDPPGAGNHSNFKMVMYHPDGDMDQSOLOQNKIKYF	180	

QY	212	RGTGAMMEVDIENGANDYLMAYALIDMDHEVINELRMGWYNTTJLMDGRIDAVNH	271
Db	181	RGTGAMMEVDTEGANDYLMAYADVDMDHPEVIELHRMGWYNTTJLMDGRIDAVNH	240
QY	272	IKSYSTRDMLTHVRNTTGKPMFAVAEFWMKNDLAAIENTYLNKTSWMNHSVEFDVPLHYLYNA	331
Db	241	IKSYSTRDMLTHVRNTTGKPMFAVAEFWMKNDLGAIENTYLNKTSWMNHSVDFDPLHYLYNA	300
QY	332	SNSGGYFDMRNLINGSVVOQKPIHAVTVPVDNHDSDQGEALSFVOSWFKPLAYALILTRE	391
Db	301	SNSGGYDMRNLINGSVVOQKPIHAVTVPVDNHDSDQGEALSFVQOQFKPLAYALILTRE	360
QY	392	QGYBSVFVFGDYGGYPTTHGVPSPMKSXIDPLQARQYAYATQMDYDPDHNDIIGTREGDSS	451
Db	361	QGYBSVFVFGADYGGYPTTHGVPSPMKSXIDPLQARQYAVATQMDYDPDHNDIIGTREGDSS	420
QY	452	HPNSGLATIMSDGPGGNKMMYVGGHKKAGOWMDITGNISGTYINADGKFNTPVNGSAVS	511
Db	421	HPNSGLATIMSDGPGGNKMMYVGGHKKAGOWMDITGNRTGYVINADGKFNTPVNGSAVS	480
QY	512	VWVKQ 516	
Db	481	VWVKQ 485	

RESULT 9

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US-08-683-838A-12
: Sequence 12, Application US/08683838A
: Patent No. 6022724
: GENERAL INFORMATION:
: APPLICANT: Svendsen, Allan
: APPLICANT: Bisg rd-Frantzen, Henrik
: APPLICANT: Borchert, Torben Vedel
: TITLE OF INVENTION: '-Amylase Mutants
: NUMBER OF SEQUENCES: 13
: CORRESPONDENCE ADDRESS:
: ADDRESSSE: No. 60222740 No. 6022724disk of No. 6022724ch America, Inc.
: STREET: 405 Lexington Avenue, 64th Floor
: CITY: New York
: STATE: New York
: COUNTRY: United States of America
: ZIP: 10174-6401
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/683,838A
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/600,908
: FILING DATE: 13-FEB-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Green, Reza
: REGISTRATION NUMBER: 38,475
: REFERENCE/DOCKET NUMBER: 4394.204-US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-867-0123
: TELEFAX: 212-878-9655
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 485 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-683-838A-12

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Query Match	91.3%	Score 2613;	DB 3:	Length 485;
Best Local Similarity	95.1%	Pred. No. 3.7e-228;		
Matches 461; Conservative	16;	Mismatches 8;	Indels 0;	Gaps 0;

Qy	32	HNHGXTGTMQVFEEMTLPRDGNHNRRLRDADANLSKSKI7AWMI.PPAMKGTSGQNDVGYGA	91
Db	1	HNHGXTGTMQVFEWTLPRDGNHNRRLDADANLSKSKI7AWMI.PPAMKGTSGQNDVGYGA	60
Qy	92	YDL.YDL.GEENQKGTVATKYGTRSLQAGVATSLKNNGLQVGYD.VYMNHGKADGETMYNAV	151
Db	61	YDL.YDL.GEENQKGTVATKYGTRSLQAGVATSLKNNGLQVGYD.VYMNHGKADGETIYNNAV	120
Qy	152	EVRNSNRNOEISGEYTIEMATKDFEPGGRNTHSNFKMRYHPFDGTDMDQSOLO.NKI.YKF	211
Db	121	EVRNSNRNOETSEYALIEAMTKDFEPGGRNNHSSFKMRYHPFDGTDMDQSOLO.NKI.YKF	180
Qy	212	RGTGKAMDEVDIENGNYDLYADI.DMDHEVYNELNMGVWYTNLT.LNDGFRIDA.VKI	271
Db	181	RGTGKAMDEVDIENGNYDLYADYDMDHEVYHELNMGVWYTNLT.LNDGFRIDA.VKI	240
Qy	272	IKTSYRDWMLTHVRNTTGGKPMFVADE.FPMKNDLALAE.NTLKTSNNHNSYFDPVPLEY.NI.YNA	331
Db	241	IKTSYFRDMLTHVRNTTGGKPMFVADE.FPMKNDLALAE.NTLKTSNNHNSYFDPVPLEY.NI.YNA	300
Qy	332	SNSGGYFEDMKNTLNGSVQKHP.LIHA.VT.PVNDHDSQPGEALBS.FVQSMFKPLAVAL.ILTRE	391
Db	301	SNSGGYDMDKNTLNGSVQKHP.LIHA.VT.EVDNHDSSQPGEALBS.FVQMKFKPLAVAL.ILTRE	360
Qy	392	QGPSPVEYGDYGI.PTHGVPSMKSKTIDP.LLQKQRYAAGTGHDXVDPDHDHDIIGMRRBEDSS	451
Db	361	QGPSPVEYGDYGI.PTHGVPSMKSKTIDP.LLQKQRYAAGTGHDXVDPDHDHDIIGMRRBEDSS	420
Qy	452	HPNSGLATTINSDPGGNKMMYYGVKHNAGQVWMDITGNRSGTIVTINADGWNFTYVNGGAVS	511
Db	421	HPNSGLATTINSDPGGNKMMYYGVKHNAGQVWMDITGNRSGTIVTINADGWNFTSVNGGAVS	480
Qy	512	VWYKQ 516	
Db	481	VWYKQ 485	

RESULT 10
US-08-600-656-1
Sequence 1, Application US/08600656
Patent No. 6093562
GENERAL INFORMATION:
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESSES:
ADDRESSEE: No. 60935620 No. 6093562disk of No. 6093562th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/600,656
FILING DATE: 13-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4338.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ. ID NO.: 1:
LENGTH: 485 amino acids

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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-600-656-1

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Query Match	91.3%	Score 2613	DB 3	Length 485
Best Local Similarity	95.1%	Pred. NO. 3.7e-228		
Matches 461	Conservative 16	Mismatches 8	Indels 0	Gaps 0

Qy	32	HNHNTNSTMMQYFEMHMLPNDGNHNNRLLRDDAANLKSXGILTAVMIPEPAKGSQNDVGVGA	91
Db	1	HNHNTNGTMMQYFEMWYLPNDGNHNNRLLRDDAANLKSXGILTAVMIPEPAKGSQNDVGVGA	60
Qy	92	YDLYDLGBFNQKGTVRTRKYGTRSQLQGAUTSLKNNGLQYGDVYMNHKGADGTEMNVAV	151
Db	61	YDLYDLGBFNQKGTVRTRKYGTRNQLAAVYSLKNNGLQYGDVYMNHKGADGTEIUNAV	120
Qy	152	EVNKSNNNOEISGEYITEAWTKPDPGGKGNHSFKRMWYHFDGTDWQSQLOKXIKYF	211
Db	121	EVNRSNNNOEISGEYIALEAWTKPDPGGKGNHSSFMRWYHFDGTDWQSQLOKXIKYF	180
Qy	212	RGTGRAMDWEVDIENGNYDYLMYADIMDHEVINELRNWGWYTNLTNLDFRIDAYKH	271
Db	181	RGTGRAMDWEVDYENGVYDYLMYADVMDHDEVIHELERNMGWYTNLTNLDFRIDAYKH	240
Qy	272	IKYSYTDWMLTHVANTTGKPMFAVALEPMKNDLAIENYLNKTSNMNHSFEVDPLAHNLVNA	331
Db	241	IKYSFTDWMILHVANNTTGKPMFAVALEPMKNDLGAIENTLNKTSNMNHSFEVDPLAHNLVNA	300
Qy	332	SNSGGYDPMRNIILNGSVVQKAPIHAVTFVDNHDSQPGEALESFVQSWKPLAYALITRE	391
Db	301	SNSGGYDPMRNIILNGSVVQKAPTAATVFVDNHDSQPGEALESFVQSWKPLAYALITRE	360
Qy	392	QGYSVSVFYGDYVYGLPTGCVPSMKSKIDPLAOARTVYAGTODHDFDHHDIIGMTRBEGSS	451
Db	361	QGYSVSVFYGDYVYGLPTGCVPSMKSKIDPLAOROTFAVGTDHDFDHHDIIGMTRBEGSS	420
Qy	452	HPNSGLATINSDGPGKNKMVYVQKHKAGQVWRDITGNBSGTVTINADGMFNTVAGAVS	511
Db	421	HPNSGLATINSDGPGKNKMVYVQKHKAGQVWRDITGNBSGTVTINADGMFNFSVAGS	480
Qy	512	VWVKO 516	
Db	481	VWVKO 485	

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RESULT 11
US-09-170-670-1
; Sequence 1, Application US/09170670
; Patent No. 6187576
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgaard-Frantzen Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 5276,200-US
; CURRENT APPLICATION NUMBER: US/09/170, 670
; CURRENT FILING DATE: 1998-10-13
; EARLIER APPLICATION NUMBER: 1172/97
; EARLIER FILING DATE: 1997-10-13
; EARLIER APPLICATION NUMBER: 60/063,306
; EARLIER FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-170-670-1

Query Match          91.3%; Score 2613; DB 3; Length 485
Best Local Similarity 95.1%; Pred. No. 3.7e-228;

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Matches	461, Conservative	16, Mismatches	8, Indels	0, Gaps	0
Qy	32	HNNGTGTMMQYFEKHALPNDGNNHNRRLDDAANLKSKITAVWIPPAWKGSQNDVGYGA	91		
Dd	1	HNNGTGTMMQYFEWYTLFNDGNNHNRRLDDAANLKSKITAVWIPPAWKGSQNDVGYGA	60		
Qy	92	YDLVLGSPNQKGTATRYTGTGTSOLQGAVTSLKNNIGIYGBGVNNHHGGADGETEMNAV	151		
Dd	61	YDLVLGSPNQKGTATRYTGTGTSOLQGAVTSLKNNIGIYGBGVNNHHGGADGETEINAV	120		
Qy	152	EVNNSNRNOEISGEYITLAWTKFDFPGKGNTHSNFKRWYHPDGTMDQSRQLQNKIKYF	211		
Dd	121	EVNNSNRNOEISGEYITLAWTKFDFPGKGNTHSNFKRWYHPDGTMDQSRQLQNKIKYF	180		
Qy	212	RGTGKAMWEVDIENGANDYLMYADIDMDHPVINELRNKGWYNTNTNLNDFRIDAVKH	271		
Dd	181	RGTGKAMWEVDIENGANDYLMYADIDMDHPVINELRNKGWYNTNTNLNDFRIDAVKH	240		
Qy	272	IKSYSTRDMLTHVRNTTGTCKPMPFAVAEPWKNDLAAIENYLNKTSNMHSYFDDVPLHNTLYNA	331		
Dd	241	IKSYSTRDMLTHVRNTTGTCKPMPFAVAEPWKNDLAAIENYLNKTSNMHSYFDDVPLHNTLYNA	300		
Qy	332	SNSGGYFDMRNILNLSVVOKPHAVTFVNDHSDPGSALBSFYQSWFKPLAYALLITRE	391		
Dd	301	SNSGGYFDMRNILNLSVVOKPHAVTFVNDHSDPGSALBSFYQSWFKPLAYALLITRE	360		
Qy	392	QGYBSVFQGVYVGPPTHGVPSPKSKIDILLQARQYANAGTQHDYDHDHDIIGMTREGSS	451		
Dd	361	QGYBSVFQGVYVGPPTHGVPSPKSKIDILLQARQYANAGTQHDYDHDHDIIGMTREGSS	420		
Qy	452	HPNSGLATIMSDPGCNKMTMYVGGKAKAGVNRDITGNRSGTVIINADGMNFTVVGAVS	511		
Dd	421	HPNSGLATIMSDPGCNKMTMYVGGKAKAGVNRDITGNRSGTVIINADGMNFTVVGAVS	480		
Qy	512	VWVKQ 516			
Dd	481	VWVKQ 485			
RESULT 12					
US-09-170-670-7					
; Sequence 7, Application US/09170670					
; Patent No. 6187576					
GENERAL INFORMATION:					
APPLICANT: Svendsen, Allan					
APPLICANT: Borchert, Torben					
APPLICANT: Bisgard-Friantzen Henrik					
TITLE OF INVENTION: Alpha-Amylase Mutants					
FILE REFERENCE: 5276.200-US					
CURRENT APPLICATION NUMBER: US/09/170,670					
CURRENT FILING DATE: 1998-10-13					
EARLIER APPLICATION NUMBER: 1172/97					
EARLIER FILING DATE: 1997-10-13					
EARLIER APPLICATION NUMBER: 60/063,306					
EARLIER FILING DATE: 1997-10-28					
NUMBER OF SEQ ID NOS: 22					
SOFTWARE: FastSeq for Windows Version 3.0					
SEQ ID NO 7					
LENGTH: 485					
TYPE: PRT					
ORGANISM: Bacillus sp.					
US-09-170-670-7					

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Query Match      91.3%  Score 2613;  DB 3      Length 485;
      Similarity 95.1%  Pred. No.3.7e-22;
      Local      461;  Conservative 16;  Mismatches 8;  Indels 0;  Gaps 0;

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QY      152 EVNRSNRNOELSGEYTLIEAWTKDFEPGRGNTSHNFKRWYHFDGIDMDOSROLONKIYKR 211
Db      121 EVNRSNRNOELSGEYALIEAWTKDFDPGRGNHNSSFKRWYHFDGIDMDOSROLONKIYKR 180
QY      212 RGTGKAMDEYDIENGNYDYLMYADIDMDHPEVINELRWGWYWTNTLNLGGRIDAVKH 271
Db      181 RGTGKAMDEYDTENGNDYLMYADYVMDHPEVIEHLRWGWYWTNTLNLGGRIDAVKH 240
QY      272 IKYSTRDMLTHVRNTGKPMFAVAFPMKNDLAIENYLNKTSWNHSVFDVPLHYNLVNA 3311
Db      241 IKYSTRDMLTHVRNTGKPMFAVAFPMKNDLAIENYLNKTSWNHSVFDVPLHYNLVNA 3000
QY      332 SNSGCFEPMRNLINSSVQKPIHAYTFPDNHDSDQGEALBESFVOSWFEPLAYALLTRE 391
Db      301 SNSGCFEPMRNLINSSVQKPIHAYTFPDNHDSDQGEALBESFVQOMFEPLAYALLTRE 360
QY      392 QGPEVFGDYDYGITTHGVSPMSKSIDPLQARQYAYVOTQDHPDHHIIGTREGNBS 451
Db      361 QGPEVFGDYDYGITTHGVSPMSKSIDPLQARQYAYVOTQDHPDHHIIGTREGNBS 420
QY      452 HPSNLATIMSDPGGNKMMYGVGKKAQGVWMDITGNBSGTYTINADGKNFTVNGCAVS 511
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QY      512 VVWVKQ 516
Db      481 VVWVKQ 485

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RESULT 13
US-09-193-068-1
; Sequence 1, Application US/09193068
; Patent No. 6197565
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Kyndt, S ren
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Andersen, Carsten
; TITLE OF INVENTION: -Amylase Variants
; FILE REFERENCE: 5709.000-US
; CURRENT APPLICATION NUMBER: US/09/193,068
; CURRENT FILING DATE: 1998-11-16
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-193-068-1

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	Query Match	91.3%	Score 2613	DB 3	Length 485
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Qy	YDLVLDGFENQKGTARTKYGTRSOLOQAVTSLKNNGIOYGVGVNNHKKGAQTEWNVAV	151			
Db	61 YDLVLDGFENQKGTARTKYGTRSOLOQAVTSLKNNGIOYGVGVNNHKKGAQTEWNVAV	120			
Qy	EVNRSNRNOISGEYTIEMWTKEFDPGRGNTHSNFKRWRYHEDGTDWDQSRLOLNKIYKF	211			
Db	121 EVNRSNRNOISGEYTIEMWTKEFDPGRGNTHSNFKRWRYHEDGTDWDQSRLOLNKIYKF	180			
Qy	RGTGAMMEVDIENGNDYLMYADLIMDHDEVINELNNMGWGYNTNTLDSFRIIDAVVGH	271			
Db	181 RGTGAMMEVDIENGNDYLMYADLIMDHDEVINELNNMGWGYNTNTLDSFRIIDAVVGH	240			
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Qy 332 SNNGGYFDMKNILINGSVVOGKHPHIAVTFVDNHDSPGEALSFVQSWFKPLAYALLITRE 391
Db 301 SNNGGYFDMKNILINGSVVOGKHPHIAVTFVDNHDSPGEALSFVQSWFKPLAYALLITRE 360
Qy 392 QGYPSVFGDYGGIPIPHGVPMKSKIDPLLOAROTAYAGOHDPFHHDITGTRBGDS 451
Db 361 QGYPSVFGDYGGIPIPHGVPMKSKIDPLLOAROTAYAGOHDPFHHDITGTRBGDS 420
Qy 452 HPSNGLATIMSDPGGNKMMYVGGKHKAGVWRDITGNRSGTITINDGWNFTVNGAVS 511
Db 421 HPSNGLATIMSDPGGNKMMYVGGKHKAGVWRDITGNRSGTITINDGWNFTVNGAVS 480
Qy 512 VVWKQ 516
Db 481 VVWKQ 485
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RESULT 14
US-09-193-068-7
; Sequence 7, Application US/09193068
; Patent No. 6197565
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Kjaerulf, Soren
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Andersen, Carsten
; TITLE OF INVENTION: -Amylase Variants
; FILE REFERENCE: 5709, 000-US
; CURRENT APPLICATION NUMBER: US/09/193,068
; CURRENT FILING DATE: 1998-11-16
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 485
; TYPE: PR1
; ORGANISM: Bacillus sp.
US-09-193-068-7
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Query Match 91.3%; Score 2613; DB 3; Length 485;
Best Local Similarity 95.1%; Pred. No. 3,7e-228;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

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Db 1 HNGTNGTMMQYFEMHLPNDGNHNNRLRDDAANKSKGITAWIPPAWKGTSONDVGCGA 60
Qy 92 YDLIDGFEFNQKGTAVTKYGTGTRSOLOGAVTSLKNNGIQYGGDVVNMHKGADGTEWNAV 151
Db 61 YDLIDGFEFNQKGTAVTKYGTGTRSOLOGAVTSLKNNGIQYGGDVVNMHKGADGTEWNAV 120
Qy 152 EVNRSNRNOISGEYITLAWTKDFPGRGNTSNFKRWYHPDGTWDSROLONKIYKF 211
Db 121 EVNRSNRNOISGEYITLAWTKDFPGRGNTSNFKRWYHPDGTWDSROLONKIYKF 180
Qy 212 RGTGKAMDVEVDIENGNVYDIAMADMDHPEVINELRNMGVYTTNLTINDGFRIDAVKH 271
Db 181 RGTGKAMDVEVDIENGNVYDIAMADMDHPEVINELRNMGVYTTNLTINDGFRIDAVKH 240
Qy 272 IKTSYTRDMLTHVRNTTGGKMPFAVAEFWKNDLGALENYLNTKTSFNNHSVFDPPLHYMLYNA 331
Db 241 IKTSYTRDMLTHVRNTTGGKMPFAVAEFWKNDLGALENYLNTKTSFNNHSVFDPPLHYMLYNA 300
Qy 332 SNNGGYFDMKNILINGSVVOGKHPHIAVTFVDNHDSPGEALSFVQSWFKPLAYALLITRE 391
Db 301 SNNGGYFDMKNILINGSVVOGKHPHIAVTFVDNHDSPGEALSFVQSWFKPLAYALLITRE 360
Qy 392 QGYPSVFGDYGGIPIPHGVPMKSKIDPLLOAROTAYAGOHDPFHHDITGTRBGDS 451
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Qy 452 HPSNGLATIMSDPGGNKMMYVGGKHKAGVWRDITGNRSGTITINDGWNFTVNGAVS 511
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Qy 512 VVWKQ 516
Db 481 VVWKQ 485
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RESULT 15
US-09-183-412-1
; Sequence 1, Application US/09183412
; Patent No. 6204232
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulf, Soren
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 5368,200-US
; CURRENT APPLICATION NUMBER: US/09/183,412
; EARLIER FILING DATE: 1998-10-30
; EARLIER APPLICATION NUMBER: 60/064,662
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 60/093,234
; EARLIER FILING DATE: 1998-07-17
; EARLIER APPLICATION NUMBER: 1240/97
; EARLIER FILING DATE: 1997-10-30
; EARLIER APPLICATION NUMBER: PA 1998 00936
; EARLIER FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 485
; TYPE: PR1
; ORGANISM: Bacillus
US-09-183-412-1
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Query Match 91.3%; Score 2613; DB 3; Length 485;
Best Local Similarity 95.1%; Pred. No. 3,7e-228;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

Qy 32 HNGTNGTMMQYFEMHLPNDGNHNNRLRDDAANKSKGITAWIPPAWKGTSONDVGCGA 91
Db 1 HNGTNGTMMQYFEMHLPNDGNHNNRLRDDAANKSKGITAWIPPAWKGTSONDVGCGA 60
Qy 92 YDLIDGFEFNQKGTAVTKYGTGTRSOLOGAVTSLKNNGIQYGGDVVNMHKGADGTEWNAV 151
Db 61 YDLIDGFEFNQKGTAVTKYGTGTRSOLOGAVTSLKNNGIQYGGDVVNMHKGADGTEWNAV 120
Qy 152 EVNRSNRNOISGEYITLAWTKDFPGRGNTSNFKRWYHPDGTWDSROLONKIYKF 211
Db 121 EVNRSNRNOISGEYITLAWTKDFPGRGNTSNFKRWYHPDGTWDSROLONKIYKF 180
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Db 181 RGTGKAMDVEVDIENGNVYDIAMADMDHPEVINELRNMGVYTTNLTINDGFRIDAVKH 240
Qy 272 IKTSYTRDMLTHVRNTTGGKMPFAVAEFWKNDLGALENYLNTKTSFNNHSVFDPPLHYMLYNA 331
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Qy 332 SNNGGYFDMKNILINGSVVOGKHPHIAVTFVDNHDSPGEALSFVQSWFKPLAYALLITRE 391
Db 301 SNNGGYFDMKNILINGSVVOGKHPHIAVTFVDNHDSPGEALSFVQSWFKPLAYALLITRE 360
Qy 392 QGYPSVFGDYGGIPIPHGVPMKSKIDPLLOAROTAYAGOHDPFHHDITGTRBGDS 451
Db 361 QGYPSVFGDYGGIPIPHGVPMKSKIDPLLOAROTAYAGOHDPFHHDITGTRBGDS 420
Qy 452 HPSNGLATIMSDPGGNKMMYVGGKHKAGVWRDITGNRSGTITINDGWNFTVNGAVS 511
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Db 421 HPNSGLATIMSDGPGGNKMTYVGKXKAGQVWRDITGNRTGTITTINADGMGNFSVNGGSVS 480

OY 512 VVWKO 516

Db 481 VVWKO 485

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GenCore version 5.1.6
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OM protein - protein search, using sw model

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(without alignments)
2817.750 Million cell updates/sec

Title: US-08-952-741-2
Perfect score: 2862
Sequence: 1 MKLHNRITSVLLTLLAAVAV.....ADGWNFTNGAVSVWVKQ 516

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2862	100.0	516	9 US-09-971-611-2	Sequence 2, Appli
3	2862	100.0	516	15 US-10-399-161-8	Sequence 8, Appli
4	2613	91.3	485	9 US-09-769-864-1	Sequence 1, Appli
5	2613	91.3	485	9 US-09-769-864-7	Sequence 7, Appli
6	2613	91.3	485	9 US-09-854-346-2	Sequence 2, Appli
7	2613	91.3	485	9 US-09-902-188A-1	Sequence 1, Appli
8	2613	91.3	485	9 US-09-918-543-2	Sequence 2, Appli
9	2613	91.3	485	9 US-09-795-211-1	Sequence 1, Appli
10	2613	91.3	485	10 US-09-925-576C-2	Sequence 2, Appli
11	2613	91.3	485	14 US-10-025-648-7	Sequence 12, Appli
12	2613	91.3	485	14 US-10-184-771-12	Sequence 12, Appli
13	2613	91.3	485	15 US-10-327-837-1	Sequence 1, Appli

14	2613	91.3	485	15 US-10-327-837-7	Sequence 7, Appli
15	2613	91.3	485	15 US-10-665-667-1	Sequence 1, Appli
16	2613	91.3	485	15 US-10-665-667-7	Sequence 7, Appli
17	2613	91.3	485	15 US-10-477-725-2	Sequence 2, Appli
18	2613	91.3	485	17 US-10-926-720-12	Sequence 12, Appli
19	2613	91.3	485	17 US-10-778-469-1	Sequence 1, Appli
20	2613	91.3	485	17 US-10-980-923-1	Sequence 1, Appli
21	2613	91.3	485	17 US-10-980-923-7	Sequence 7, Appli
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24	2440	85.3	485	9 US-09-769-864-8	Sequence 8, Appli
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27	2440	85.3	485	9 US-09-918-543-2	Sequence 4, Appli
28	2440	85.3	485	9 US-09-795-211-2	Sequence 2, Appli
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35	2440	85.3	485	15 US-10-477-725-4	Sequence 4, Appli
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43	2410	84.2	485	14 US-10-025-648-7	Sequence 7, Appli
44	2410	84.2	485	15 US-10-327-837-6	Sequence 6, Appli
45	2410	84.2	485	15 US-10-665-667-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-986-676A-2
Sequence 2, Application US/09986676A
Patent No. US20020102698A1
GENERAL INFORMATION:
APPLICANT: HATADA, Yoji
APPLICANT: OZAKI, Katsuya
APPLICANT: ARA, Katsutoshi
APPLICANT: KAWAI, Shuji
APPLICANT: ITO, Susumu
TITLE OF INVENTION: Gene Encoding Alkaline Liquefying Alpha-Amylase
CURRENT APPLICATION NUMBER: US/09/986,676A
CURRENT FILING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: PCT/JP96/01641
PRIOR FILING DATE: 1996-06-14
PRIOR APPLICATION NUMBER: Japan 147257/1995
PRIOR FILING DATE: 1995-06-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 516
TYPE: PRT
ORGANISM: Bacillus sp.
US-09-986-676A-2
Query Match 100.0%; Score 2862; DB 9; Length 516;
Best Local Similarity 100.0%; Pred. No. 2, 7e-239;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MKLHNRITSVLLTLLAAVAVLPYMTBPAQAHNGTGTMMQYFEWTLPDNGHNNLRD 60
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Db 61 DAANLKSKITAVWIPPAKGTSONDVGYGAYDLVLDGEFNOKGTVRTKYGTRSQLQAV 120
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Db 121 TSLKNNGIQVYGVVNNHKGADGTEMVNAVEVNRNNOEISGEYTIEMTKFDPFGRG 180
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Db 181 NTHSNFKMRYHFDGTDWQSRLOKNIYKFRGTGKAMWEVDIENGNDYLMYADIDMD 240
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QY 481 VNRDITGNRSQVTTINADGNGFTVNGAVSVWVKQ 516
Db 481 VNRDITGNRSQVTTINADGNGFTVNGAVSVWVKQ 516

RESULT 2
US-09-971-611-2

Sequence 2, Application US/09971611
Patent No. US20020123124A1
GENERAL INFORMATION:
APPLICANT: ARAKI, HIROYUKI
APPLICANT: ENDO, KEIJI
APPLICANT: HAGIHARA, HIROSHI
APPLICANT: IGARASHI, KAZUAKI
APPLICANT: HAYASHI, YASUHIRO
APPLICANT: OZAKI, KATSUYA
TITLE OF INVENTION: HIGHLY PRODUCTIVE ALPHA-AMYLASES
FILE REFERENCE: 214377US0
CURRENT APPLICATION NUMBER: US/09/971, 611
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: JP 2000/310605
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 516
TYPE: PRN
ORGANISM: Bacillus sp. KSM-AP1378
US-09-971-611-2

Query Match 100.0%; Score 2862; DB 9; Length 516;
Best Local Similarity 100.0%; Pred. No. 2,7e-239;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 481 VNRDITGNRSQVTTINADGNGFTVNGAVSVWVKQ 516

RESULT 3
US-10-399-161-8

Sequence 8, Application US/10399161
Publication No. US20040091994A1
GENERAL INFORMATION:
APPLICANT: Andersen, Carsten
TITLE OF INVENTION: Alpha-amylase variant with altered properties
FILE REFERENCE: 10115, 204-WO
CURRENT APPLICATION NUMBER: US/10/399, 161
PRIOR FILING DATE: 2003-04-11
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.2
SEQ ID NO 8
LENGTH: 516
TYPE: PRN
ORGANISM: Bacillus sp.
US-10-399-161-8

Query Match 100.0%; Score 2862; DB 15; Length 516;
Best Local Similarity 100.0%; Pred. No. 2,7e-239;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKLHNRIISVLLTLLAVAVLPYMTPEAOAHNNGTGMQYFEWHLPRDGNHNRRLD 60
Db 1 MKLHNRIISVLLTLLAVAVLPYMTPEAOAHNNGTGMQYFEWHLPRDGNHNRRLD 60
QY 61 DAANLKSKITAVWIPPAKGTSONDVGYGAYDLVLDGEFNOKGTVRTKYGTRSQLQAV 120
Db 61 DAANLKSKITAVWIPPAKGTSONDVGYGAYDLVLDGEFNOKGTVRTKYGTRSQLQAV 120
QY 121 TSLKNNGIQVYGVVNNHKGADGTEMVNAVEVNRNNOEISGEYTIEMTKFDPFGRG 180
Db 121 TSLKNNGIQVYGVVNNHKGADGTEMVNAVEVNRNNOEISGEYTIEMTKFDPFGRG 180
QY 181 NTHSNFKMRYHFDGTDWQSRLOKNIYKFRGTGKAMWEVDIENGNDYLMYADIDMD 240
Db 181 NTHSNFKMRYHFDGTDWQSRLOKNIYKFRGTGKAMWEVDIENGNDYLMYADIDMD 240
QY 241 HPEVINELNMGVWYNTNLNDGFRIDAVKHIKYSTYRDMLTGVRNTGKPMFAVAEFWK 300
Db 241 HPEVINELNMGVWYNTNLNDGFRIDAVKHIKYSTYRDMLTGVRNTGKPMFAVAEFWK 300
QY 301 NDLAALIENTLNTSNHSHVFDVPLAHYNLYNASNSGYPFMRNLINSVVOQKPIHATFV 360
Db 301 NDLAALIENTLNTSNHSHVFDVPLAHYNLYNASNSGYPFMRNLINSVVOQKPIHATFV 360
QY 361 DNHDSPGEBALSFVQSWFKPLAYALILTRREGYPSVFYGDYGIPTHGVPMSKSIDPL 420
Db 361 DNHDSPGEBALSFVQSWFKPLAYALILTRREGYPSVFYGDYGIPTHGVPMSKSIDPL 420

Qy 421 LOARQYAYGTOHDYFDHHDIGWTRBGDSHPNSGLATIMSDPGGKMMYVGKHAKGQ 480
 Db 421 LOARQYAYGTOHDYFDHHDIGWTRBGDSHPNSGLATIMSDPGGKMMYVGKHAKGQ 480
 Qy 481 VWRDITGNRSQGVITINADGWNFTVNGCAVSVMWQ 516
 Db 481 VWRDITGNRSQGVITINADGWNFTVNGCAVSVMWQ 516

RESULT 4
 US-09-769-864-1
 ; Sequence 1, Application US/09769864
 ; Patent No. US20010039253A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Borchert, Torben V.
 ; APPLICANT: Svendsen, Allan
 ; APPLICANT: Andersen, Carsten
 ; APPLICANT: Nielsen, Bjarne
 ; APPLICANT: Nielsen, Torben L.
 ; APPLICANT: Kjaerulff, Soren
 ; TITLE OF INVENTION: Alpha-Amylase Mutants
 ; FILE REFERENCE: 5368.200-US
 ; CURRENT APPLICATION NUMBER: US/09/769,864
 ; PRIOR FILING DATE: 2001-01-25
 ; PRIOR APPLICATION NUMBER: 09/183,412
 ; PRIOR FILING DATE: 1998-10-30
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 485
 ; TYPE: PRF
 ; ORGANISM: Bacillus
 ; US-09-769-864-1

Query Match 91.3%; Score 2613; DB 9; Length 485;
 Best Local Similarity 95.1%; Pred. No. 9.7e-218;
 Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

Qy 32 HHNGTNGTMMQYFEWHLIPNDGNHNRRLRDAANLKSIGITAWIPPMWKGTSQNDVGYGA 91
 Db 1 HHNGTNGTMMQYFEWHLIPNDGNHNRRLRDAANLKSIGITAWIPPMWKGTSQNDVGYGA 60
 Qy 92 YDLIDLSEFNOKGVRKRYGTRSOLOGAVTSLKNGIIOYGDVVMNHKGADGTEIMNAV 151
 Db 61 YDLIDLSEFNOKGVRKRYGTRSOLOGAVTSLKNGIIOYGDVVMNHKGADGTEIMNAV 120
 Qy 152 EVNRSNNOBISGEYTIEMTKFDPGKGNTHSNFKRWYHFDGTDMDQSRQLOKNTYKF 211
 Db 121 EVNRSNNOBISGEYTIEMTKFDPGKGNTHSNFKRWYHFDGTDMDQSRQLOKNTYKF 180
 Qy 212 RGCGKAMDWEVDLENGYDYIMADIMDHEVINELRNNGWYTNLTINLDFRIDAVKH 271
 Db 181 RGCGKAMDWEVDLENGYDYIMADIMDHEVINELRNNGWYTNLTINLDFRIDAVKH 240
 Qy 272 IKSYTRDMTLTHVNTTGKMPFAVAEFWKNDLAIENYLNKTSWNHNVFDPVPLHYNLXNA 331
 Db 241 IKSYTRDMTLTHVNTTGKMPFAVAEFWKNDLAIENYLNKTSWNHNVFDPVPLHYNLXNA 300
 Qy 332 SNNGGYEDMNIILNGSVVQKHPPIHAYTFVNDHDSQPEALESPVQWFKPLAVALILTRE 391
 Db 301 SNNGGYEDMNIILNGSVVQKHPPIHAYTFVNDHDSQPEALESPVQWFKPLAVALILTRE 360
 Qy 392 QGYPVSFYGDYIGYPTHGVPMSKSIDPLLOARQTYAYGTOHDYFDHHDIGWTRBGDS 451
 Db 361 QGYPVSFYGDYIGYPTHGVPMSKSIDPLLOARQTYAYGTOHDYFDHHDIGWTRBGDS 420
 Qy 452 HPNSGLATIMSDPGGKMMYVGKHAKGQVWRDITGNRSQGVITINADGWNFTVNGCAVS 511
 Db 421 HPNSGLATIMSDPGGKMMYVGKHAKGQVWRDITGNRSQGVITINADGWNFTVNGCAVS 480
 Qy 512 VVWQ 516
 Db 512 VVWQ 516

Db 481 VVWQ 485
 RESULT 5
 US-09-769-864-7
 ; Sequence 7, Application US/09769864
 ; Patent No. US20010039253A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Borchert, Torben V.
 ; APPLICANT: Svendsen, Allan
 ; APPLICANT: Andersen, Carsten
 ; APPLICANT: Nielsen, Bjarne
 ; APPLICANT: Nielsen, Torben L.
 ; APPLICANT: Kjaerulff, Soren
 ; TITLE OF INVENTION: Alpha-Amylase Mutants
 ; FILE REFERENCE: 5368.200-US
 ; CURRENT APPLICATION NUMBER: US/09/769,864
 ; PRIOR FILING DATE: 2001-01-25
 ; PRIOR APPLICATION NUMBER: 09/183,412
 ; PRIOR FILING DATE: 1998-10-30
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 7
 ; LENGTH: 485
 ; TYPE: PRF
 ; ORGANISM: Bacillus sp.
 ; US-09-769-864-7

Query Match 91.3%; Score 2613; DB 9; Length 485;
 Best Local Similarity 95.1%; Pred. No. 9.7e-218;
 Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

Qy 32 HHNGTNGTMMQYFEWHLIPNDGNHNRRLRDAANLKSIGITAWIPPMWKGTSQNDVGYGA 91
 Db 1 HHNGTNGTMMQYFEWHLIPNDGNHNRRLRDAANLKSIGITAWIPPMWKGTSQNDVGYGA 60
 Qy 92 YDLIDLSEFNOKGVRKRYGTRSOLOGAVTSLKNGIIOYGDVVMNHKGADGTEIMNAV 151
 Db 61 YDLIDLSEFNOKGVRKRYGTRSOLOGAVTSLKNGIIOYGDVVMNHKGADGTEIMNAV 120
 Qy 152 EVNRSNNOBISGEYTIEMTKFDPGKGNTHSNFKRWYHFDGTDMDQSRQLOKNTYKF 211
 Db 121 EVNRSNNOBISGEYTIEMTKFDPGKGNTHSNFKRWYHFDGTDMDQSRQLOKNTYKF 180
 Qy 212 RGCGKAMDWEVDLENGYDYIMADIMDHEVINELRNNGWYTNLTINLDFRIDAVKH 271
 Db 181 RGCGKAMDWEVDLENGYDYIMADIMDHEVINELRNNGWYTNLTINLDFRIDAVKH 240
 Qy 272 IKSYTRDMTLTHVNTTGKMPFAVAEFWKNDLAIENYLNKTSWNHNVFDPVPLHYNLXNA 331
 Db 241 IKSYTRDMTLTHVNTTGKMPFAVAEFWKNDLAIENYLNKTSWNHNVFDPVPLHYNLXNA 300
 Qy 332 SNNGGYEDMNIILNGSVVQKHPPIHAYTFVNDHDSQPEALESPVQWFKPLAVALILTRE 391
 Db 301 SNNGGYEDMNIILNGSVVQKHPPIHAYTFVNDHDSQPEALESPVQWFKPLAVALILTRE 360
 Qy 392 QGYPVSFYGDYIGYPTHGVPMSKSIDPLLOARQTYAYGTOHDYFDHHDIGWTRBGDS 451
 Db 361 QGYPVSFYGDYIGYPTHGVPMSKSIDPLLOARQTYAYGTOHDYFDHHDIGWTRBGDS 420
 Qy 452 HPNSGLATIMSDPGGKMMYVGKHAKGQVWRDITGNRSQGVITINADGWNFTVNGCAVS 511
 Db 421 HPNSGLATIMSDPGGKMMYVGKHAKGQVWRDITGNRSQGVITINADGWNFTVNGCAVS 480
 Qy 512 VVWQ 516
 Db 481 VVWQ 485

RESULT 6
 US-09-854-346-2
 ; Sequence 2, Application US/09854346
 ; Patent No. US20020068352A1

GENERAL INFORMATION:
 APPLICANT: No. US20020068352A1ozymes A/S
 APPLICANT: Svendsen, Allan
 APPLICANT: Jorgensen, Christel Thea
 APPLICANT: Nielsen, Bjarne Ronfeldt
 TITLE OF INVENTION: Alpha-amylase variants with altered 1,6 activity
 FILE REFERENCE: 6140.200-US
 CURRENT APPLICATION NUMBER: US/09/854,346
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: PatentIn version 3.1
 SEQ. ID NO. 2
 LENGTH: 485
 TYPE: PRT
 ORGANISM: Bacillus sp.
 US-09-854-346-2

Query Match 91.3%; Score 2613; DB 9; Length 485;
 Best Local Similarity 95.1%; Pred. No. 9.7e-218;
 Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

32 HNGTNGTMMQYFEWMLPNDGNHNRRLRDAANLKSKITAVWIPAMKGTSONDVYGA 91
 1 HNGTNGTMMQYFEWMLPNDGNHNRRLRDAANLKSKITAVWIPAMKGTSONDVYGA 60
 92 YDIYDIYGEFNQKGTVRTKGTGTSOLQCAVTSLKNGIOYVGVVNMHKGAGDTEVNAV 151
 61 YDIYDIYGEFNQKGTVRTKGTGTSOLQCAVTSLKNGIOYVGVVNMHKGAGDTEVNAV 120
 152 EVNRSNRNOISGEYTIEMTKFDPGRGNTHSNFKRWYHFDGTDMDOSROLONKIYKF 211
 121 EVNRSNRNOISGEYTIEMTKFDPGRGNTHSNFKRWYHFDGTDMDOSROLONKIYKF 180
 212 RGTGKAMDEVDIENGNYDYLMTADIDMDHPEVINELRWGWYTYTTLNDGFRIDAVKH 271
 181 RGTGKAMDEVDIENGNYDYLMTADIDMDHPEVINELRWGWYTYTTLNDGFRIDAVKH 240
 272 IKSYSTRDMLTHVRNTGKMPFAVAEFWKNDLAIENYLNKTSWNHVSFVDPPLHYLYNA 331
 241 IKSYSTRDMLTHVRNTGKMPFAVAEFWKNDLAIENYLNKTSWNHVSFVDPPLHYLYNA 300
 332 SMSGGYFDMNINLNGSVVQKPHAVTFVNDHDSQGEALLESFVQSFKFLAYALILTRE 391
 301 SMSGGYFDMNINLNGSVVQKPHAVTFVNDHDSQGEALLESFVQSFKFLAYALILTRE 360
 392 QGYPSVFEYDYGIPHTGVPMSKSIDPLLOARQTYAYGTQHDYFDHDIIGWTRGDS 451
 361 QGYPSVFEYDYGIPHTGVPMSKSIDPLLOARQTYAYGTQHDYFDHDIIGWTRGDS 420
 452 HPSNGLATIMSDGPGKMKMYVGHKAGOWWRDITGNRSQTYITINADGNGNFTVNGGAVS 511
 421 HPSNGLATIMSDGPGKMKMYVGHKAGOWWRDITGNRSQTYITINADGNGNFTVNGGAVS 480
 512 VWYKQ 516
 481 VWYKQ 485

RESULT 7
 US-09-902-188A-1
 Sequence 1, Application US/09902188A
 Patent No. US2002009896A1
 GENERAL INFORMATION:
 APPLICANT: Bisgaard-Frantzen, Henrik
 Svendsen, Allan
 Borchert, Torben Vedel
 TITLE OF INVENTION: AMYLASE VARIANTS
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. US2002009896A1o No. US2002009896A1disk of No. US200200985
 STREET: 405 Lexington Avenue, Suite 6400
 CITY: New York
 STATE: New York

COUNTRY: U.S.A.
 ZIP: 10174-6401
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/902,188A
 FILING DATE: 10-Jul-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/354,191
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Lambitis, Elias J.
 REGISTRATION NUMBER: 33,728
 REFERENCE/DOCKET NUMBER: 4318.204-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 867 0123
 TELEFAX: 212 867 0298
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 485 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-09-902-188A-1

Query Match 91.3%; Score 2613; DB 9; Length 485;
 Best Local Similarity 95.1%; Pred. No. 9.7e-218;
 Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

32 HNGTNGTMMQYFEWMLPNDGNHNRRLRDAANLKSKITAVWIPAMKGTSONDVYGA 91
 1 HNGTNGTMMQYFEWMLPNDGNHNRRLRDAANLKSKITAVWIPAMKGTSONDVYGA 60
 92 YDIYDIYGEFNQKGTVRTKGTGTSOLQCAVTSLKNGIOYVGVVNMHKGAGDTEVNAV 151
 61 YDIYDIYGEFNQKGTVRTKGTGTSOLQCAVTSLKNGIOYVGVVNMHKGAGDTEVNAV 120
 152 EVNRSNRNOISGEYTIEMTKFDPGRGNTHSNFKRWYHFDGTDMDOSROLONKIYKF 211
 121 EVNRSNRNOISGEYTIEMTKFDPGRGNTHSNFKRWYHFDGTDMDOSROLONKIYKF 180
 212 RGTGKAMDEVDIENGNYDYLMTADIDMDHPEVINELRWGWYTYTTLNDGFRIDAVKH 271
 181 RGTGKAMDEVDIENGNYDYLMTADIDMDHPEVINELRWGWYTYTTLNDGFRIDAVKH 240
 272 IKSYSTRDMLTHVRNTGKMPFAVAEFWKNDLAIENYLNKTSWNHVSFVDPPLHYLYNA 331
 241 IKSYSTRDMLTHVRNTGKMPFAVAEFWKNDLAIENYLNKTSWNHVSFVDPPLHYLYNA 300
 332 SMSGGYFDMNINLNGSVVQKPHAVTFVNDHDSQGEALLESFVQSFKFLAYALILTRE 391
 301 SMSGGYFDMNINLNGSVVQKPHAVTFVNDHDSQGEALLESFVQSFKFLAYALILTRE 360
 392 QGYPSVFEYDYGIPHTGVPMSKSIDPLLOARQTYAYGTQHDYFDHDIIGWTRGDS 451
 361 QGYPSVFEYDYGIPHTGVPMSKSIDPLLOARQTYAYGTQHDYFDHDIIGWTRGDS 420
 452 HPSNGLATIMSDGPGKMKMYVGHKAGOWWRDITGNRSQTYITINADGNGNFTVNGGAVS 511
 421 HPSNGLATIMSDGPGKMKMYVGHKAGOWWRDITGNRSQTYITINADGNGNFTVNGGAVS 480
 512 VWYKQ 516
 481 VWYKQ 485

RESULT 8

US-09-918-543-2
 ; Sequence 2, Application US/09918543
 ; Patent No. US20020155574A1
 ; GENERAL INFORMATION:
 ; APPLICANT: No. US20020155574A1ozymes A/S
 ; APPLICANT: Thisted, Thomas
 ; APPLICANT: Kjaerulf, Soren
 ; APPLICANT: Andersen, Carsten
 ; APPLICANT: Fuglaang, Claus Crone
 ; TITLE OF INVENTION: Alpha-amylase mutants with altered properties
 ; FILE REFERENCE: 10062.200-US
 ; CURRENT APPLICATION NUMBER: US/09/918,543
 ; CURRENT FILING DATE: 2001-07-31
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 485
 ; TYPE: PRT
 ; ORGANISM: Bacillus sp.
 ; US-09-918-543-2

Query Match 91.3%; Score 2613; DB 9; Length 485;
 Best Local Similarity 95.1%; Pred. No. 9.7e-218;
 Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

Qy 32 HHNGTNGTMMQYFEMHLPNDGNHNRRLRDAANLKSIGITAVWI.PPAMKGTSONDVGYGA 91
 Db 1 HHNGTNGTMMQYFEMHLPNDGNHNRRLRDAANLKSIGITAVWI.PPAMKGTSONDVGYGA 60
 Qy 92 YDLVDLGEFNOKGTVRTKYGTGRSOLQGAVTSLKNNGLQVYGDVVMNHKGGADGTEMVNAV 151
 Db 61 YDLVDLGEFNOKGTVRTKYGTGRNOLQAAVTSLKNNGLQVYGDVVMNHKGGADGTEIYNVAV 120
 Qy 152 EVNRSNRNOEISGEYTTIEMTKFDPGKGNTHSNFKRWYHFDGTDWDQSRLOLNKIYKF 211
 Db 121 EVNRSNRNOEISGEYTTIEMTKFDPGKGNTHSNFKRWYHFDGTDWDQSRLOLNKIYKF 180
 Qy 212 RGTGKADMEVDINGNVDYLMYADVDMDHPEVINELRNMGVWYTNLTNLNDFRIDAVKH 271
 Db 181 RGTGKADMEVDINGNVDYLMYADVDMDHPEVINELRNMGVWYTNLTNLNDFRIDAVKH 240
 Qy 272 IKYSYTRDMLTHVANTTGKPMFAVAEFKNDLAAIENYLNKTSNNHSHVFDVPLHYNLXNA 331
 Db 241 IKYSYTRDMLTHVANTTGKPMFAVAEFKNDLAAIENYLNKTSNNHSHVFDVPLHYNLXNA 300
 Qy 332 SNSGGYEDMNRILNLSVVOQKPIHAAVTVDNHSQPEALESFYQSWFKPLAVALILTRE 391
 Db 301 SNSGGYEDMNRILNLSVVOQKPIHAAVTVDNHSQPEALESFYQSWFKPLAVALILTRE 360
 Qy 392 QGYSVFVGYDYGGI.PTHGVPMKSKIDPLQAROTYAVGTQHDYFDHDDIIGWTRBGSS 451
 Db 361 QGYSVFVGYDYGGI.PTHGVPMKSKIDPLQAROTYAVGTQHDYFDHDDIIGWTRBGSS 420
 Qy 452 HPNSGLATIMSDGPGKMMYVGGKAKAGVWRDITGNRSGLTITNADGNGFTVNGGAVS 511
 Db 421 HPNSGLATIMSDGPGKMMYVGGKAKAGVWRDITGNRSGLTITNADGNGFTVNGGAVS 480
 Qy 512 VVWVQ 516
 Db 481 VVWVQ 485

RESULT 9
 US-09-795-211-1
 ; Sequence 1, Application US/09795211
 ; Publication No. US20020183226A1
 ; GENERAL INFORMATION:
 ; APPLICANT: The Procter & Gamble Company
 ; APPLICANT: Kaesturi, Chandrika
 ; APPLICANT: Wandersat, Mark E.
 ; APPLICANT: Song, Brian X.
 ; TITLE OF INVENTION: LIQUID DETERGENT COMPOSITION EXHIBITING ENHANCED a-AMYLASE ENZYME
 ; TITLE OF INVENTION: STABILITY

FILE REFERENCE: Detergent Composition
 ; CURRENT APPLICATION NUMBER: US/09/795,211
 ; CURRENT FILING DATE: 2001-02-28
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 485
 ; TYPE: PRT
 ; ORGANISM: alkaliphilicobacillus
 ; US-09-795-211-1

Query Match 91.3%; Score 2613; DB 9; Length 485;
 Best Local Similarity 95.1%; Pred. No. 9.7e-218;
 Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

Qy 32 HHNGTNGTMMQYFEMHLPNDGNHNRRLRDAANLKSIGITAVWI.PPAMKGTSONDVGYGA 91
 Db 1 HHNGTNGTMMQYFEMHLPNDGNHNRRLRDAANLKSIGITAVWI.PPAMKGTSONDVGYGA 60
 Qy 92 YDLVDLGEFNOKGTVRTKYGTGRSOLQGAVTSLKNNGLQVYGDVVMNHKGGADGTEMVNAV 151
 Db 61 YDLVDLGEFNOKGTVRTKYGTGRNOLQAAVTSLKNNGLQVYGDVVMNHKGGADGTEIYNVAV 120
 Qy 152 EVNRSNRNOEISGEYTTIEMTKFDPGKGNTHSNFKRWYHFDGTDWDQSRLOLNKIYKF 211
 Db 121 EVNRSNRNOEISGEYTTIEMTKFDPGKGNTHSNFKRWYHFDGTDWDQSRLOLNKIYKF 180
 Qy 212 RGTGKADMEVDINGNVDYLMYADVDMDHPEVINELRNMGVWYTNLTNLNDFRIDAVKH 271
 Db 181 RGTGKADMEVDINGNVDYLMYADVDMDHPEVINELRNMGVWYTNLTNLNDFRIDAVKH 240
 Qy 272 IKYSYTRDMLTHVANTTGKPMFAVAEFKNDLAAIENYLNKTSNNHSHVFDVPLHYNLXNA 331
 Db 241 IKYSYTRDMLTHVANTTGKPMFAVAEFKNDLAAIENYLNKTSNNHSHVFDVPLHYNLXNA 300
 Qy 332 SNSGGYEDMNRILNLSVVOQKPIHAAVTVDNHSQPEALESFYQSWFKPLAVALILTRE 391
 Db 301 SNSGGYEDMNRILNLSVVOQKPIHAAVTVDNHSQPEALESFYQSWFKPLAVALILTRE 360
 Qy 392 QGYSVFVGYDYGGI.PTHGVPMKSKIDPLQAROTYAVGTQHDYFDHDDIIGWTRBGSS 451
 Db 361 QGYSVFVGYDYGGI.PTHGVPMKSKIDPLQAROTYAVGTQHDYFDHDDIIGWTRBGSS 420
 Qy 452 HPNSGLATIMSDGPGKMMYVGGKAKAGVWRDITGNRSGLTITNADGNGFTVNGGAVS 511
 Db 421 HPNSGLATIMSDGPGKMMYVGGKAKAGVWRDITGNRSGLTITNADGNGFTVNGGAVS 480
 Qy 512 VVWVQ 516
 Db 481 VVWVQ 485

RESULT 10
 US-09-925-576C-2
 ; Sequence 2, Application US/09925576C
 ; Publication No. US20030129718A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Andersen, Carsten
 ; APPLICANT: Borchert, Torben Vedel
 ; APPLICANT: Nielsen, Bjarne Ronfeldt
 ; TITLE OF INVENTION: Amylase Variants
 ; FILE REFERENCE: 10004.204-US
 ; CURRENT APPLICATION NUMBER: US/09/925,576C
 ; CURRENT FILING DATE: 2001-08-09
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 485
 ; TYPE: PRT
 ; ORGANISM: Bacillus sp.
 ; US-09-925-576C-2

Query Match 91.3%; Score 2613; DB 10; Length 485;

Best Local Similarity 95.1%; Pred. No. 9,7e-218;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

```
QY 32 HHNGTGMQYFEWHLFNDGNHNRRLRDDAANLKSKITAVWIPPAWKGTSONDVGYCA 91
DB 1 HHNGTGMQYFEWHLFNDGNHNRRLRDDAANLKSKITAVWIPPAWKGTSONDVGYCA 60
QY 92 YDLYDGEFNQKGTVRTKXGTSOQAGATSLKNNGIQYGVVMMHKGAGDTELVNAV 151
DB 61 YDLYDGEFNQKGTVRTKXGTSOQAGATSLKNNGIQYGVVMMHKGAGDTELVNAV 120
QY 152 EVNRSNRNOEISEGYTIEAWTKFDFPGRGNTSHNFKRWYHFDGTDMDOSROLQNKIYKF 211
DB 121 EVNRSNRNOEISEGYTIEAWTKFDFPGRGNTSHNFKRWYHFDGTDMDOSROLQNKIYKF 180
QY 212 RGTGKAMDEVDIENGNDYLMADIDMDHPEVINELRNMGWYNTNLMDGFRIDAVKH 271
DB 181 RGTGKAMDEVDIENGNDYLMADIDMDHPEVINELRNMGWYNTNLMDGFRIDAVKH 240
QY 272 IKYSYTRDMLTHVRNTTGKMPFAVAEFWKNDLALIENTYLNKTSNMHSVPDPLHYNLNA 331
DB 241 IKYSYTRDMLTHVRNTTGKMPFAVAEFWKNDLALIENTYLNKTSNMHSVPDPLHYNLNA 300
QY 332 SNSGGYFDMRNILNGSVQKHPIHAYTFVNDHDSQGEALSFVQSWFKPLAYALVLTRE 391
DB 301 SNSGGYFDMRNILNGSVQKHPIHAYTFVNDHDSQGEALSFVQSWFKPLAYALVLTRE 360
QY 392 QGYPSVFGDYGIPIPHGVPSMKSIDPLLOARQTYAYGTQHDYFDHDIIGTREGDSS 451
DB 361 QGYPSVFGDYGIPIPHGVPSMKSIDPLLOARQTYAYGTQHDYFDHDIIGTREGDSS 420
QY 452 HPNSGLATTMSDGPGRKMMYVGKHKAGVWRDITGNBSGTVTINADGKNFTVNGGAVS 511
DB 421 HPNSGLATTMSDGPGRKMMYVGKHKAGVWRDITGNBSGTVTINADGKNFTVNGGAVS 480
QY 512 VVWKQ 516
DB 481 VVWKQ 485
```

RESULT 11
US-10-025-648-1
; Sequence 1, Application US/10025648
; Publication No. US20030064908A1
; GENERAL INFORMATION:

APPLICANT: Bisgaard-Frantzen, Henrik
Svendsen, Allan
Borchert, Torden Vedel
TITLE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Novo Nordisk of North America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/025,648
FILING DATE: 19-Dec-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/600,656
FILING DATE: 13-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4318, 204-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-025-648-1

Query Match 91.3%; Score 2613; DB 14; Length 485;
Best Local Similarity 95.1%; Pred. No. 9,7e-218;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

```
QY 32 HHNGTGMQYFEWHLFNDGNHNRRLRDDAANLKSKITAVWIPPAWKGTSONDVGYCA 91
DB 1 HHNGTGMQYFEWHLFNDGNHNRRLRDDAANLKSKITAVWIPPAWKGTSONDVGYCA 60
QY 92 YDLYDGEFNQKGTVRTKXGTSOQAGATSLKNNGIQYGVVMMHKGAGDTELVNAV 151
DB 61 YDLYDGEFNQKGTVRTKXGTSOQAGATSLKNNGIQYGVVMMHKGAGDTELVNAV 120
QY 152 EVNRSNRNOEISEGYTIEAWTKFDFPGRGNTSHNFKRWYHFDGTDMDOSROLQNKIYKF 211
DB 121 EVNRSNRNOEISEGYTIEAWTKFDFPGRGNTSHNFKRWYHFDGTDMDOSROLQNKIYKF 180
QY 212 RGTGKAMDEVDIENGNDYLMADIDMDHPEVINELRNMGWYNTNLMDGFRIDAVKH 271
DB 181 RGTGKAMDEVDIENGNDYLMADIDMDHPEVINELRNMGWYNTNLMDGFRIDAVKH 240
QY 272 IKYSYTRDMLTHVRNTTGKMPFAVAEFWKNDLALIENTYLNKTSNMHSVPDPLHYNLNA 331
DB 241 IKYSYTRDMLTHVRNTTGKMPFAVAEFWKNDLALIENTYLNKTSNMHSVPDPLHYNLNA 300
QY 332 SNSGGYFDMRNILNGSVQKHPIHAYTFVNDHDSQGEALSFVQSWFKPLAYALVLTRE 391
DB 301 SNSGGYFDMRNILNGSVQKHPIHAYTFVNDHDSQGEALSFVQSWFKPLAYALVLTRE 360
QY 392 QGYPSVFGDYGIPIPHGVPSMKSIDPLLOARQTYAYGTQHDYFDHDIIGTREGDSS 451
DB 361 QGYPSVFGDYGIPIPHGVPSMKSIDPLLOARQTYAYGTQHDYFDHDIIGTREGDSS 420
QY 452 HPNSGLATTMSDGPGRKMMYVGKHKAGVWRDITGNBSGTVTINADGKNFTVNGGAVS 511
DB 421 HPNSGLATTMSDGPGRKMMYVGKHKAGVWRDITGNBSGTVTINADGKNFTVNGGAVS 480
QY 512 VVWKQ 516
DB 481 VVWKQ 485
```

RESULT 12
US-10-184-771-12
; Sequence 12, Application US/10184771
; Publication No. US20030170769A1
; GENERAL INFORMATION:

APPLICANT: Svendsen, Allan
Borchert, Torden Vedel
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 076/1F216-US2
CURRENT APPLICATION NUMBER: US/10/184,771
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US/09/636,252
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 08/683,838
PRIOR FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FaelsSeq for Windows Version 3.0
; SEQ ID NO 12

LENGTH: 485
TYPE: PRT
ORGANISM: Bacillus
US-10-184-771-12

Query Match 91.3%; Score 2613; DB 14; Length 485;
Best Local Similarity 95.1%; Pred. No. 9.7e-218;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

```

Qy 32 HHNGTGMQYEFMHLNDGNHNRRLRDDAANKSKGITAVWIPPAKGTSONDVGYGA 91
Db 1 HHNGTGMQYEFMHLNDGNHNRRLRDDAANKSKGITAVWIPPAKGTSONDVGYGA 60
Qy 92 YDLVDLGEFNQKGVRTKYGTRNQLAAVTSLKNGIIOVGDVNMNHKGADGTEIVNAV 151
Db 61 YDLVDLGEFNQKGVRTKYGTRNQLAAVTSLKNGIIOVGDVNMNHKGADGTEIVNAV 120
Qy 152 EVNSNRNOEISGEYTIEMWTKFDFPGKGNTHSNFKRWYHFDGTDMDQSRQLONKIYKF 211
Db 121 EVNSNRNOEISGEYTIEMWTKFDFPGKGNTHSNFKRWYHFDGTDMDQSRQLONKIYKF 180
Qy 212 RGTGKAMDWEVDENGNVDYLMYADVMDHBEVHIELRMGWYNTLTLNDGFRIDA VKH 271
Db 181 RGTGKAMDWEVDENGNVDYLMYADVMDHBEVHIELRMGWYNTLTLNDGFRIDA VKH 240
Qy 272 IKSYTRDMLTHVNTTGGKPMFAVAEFWKNDLAIENYLNKTSWNHSEVDVPLHYNL YNA 331
Db 241 IKSYTRDMLTHVNTTGGKPMFAVAEFWKNDLAIENYLNKTSWNHSEVDVPLHYNL YNA 300
Qy 332 SNSGGEYDMRNILNGSVQKPIHAAVTFVDNHDSQPEALESFYQSWFKPLAVALITRE 391
Db 301 SNSGGEYDMRNILNGSVQKPIHAAVTFVDNHDSQPEALESFYQSWFKPLAVALITRE 360
Qy 392 QGYPSVFGDYGGIPIHGVBSMKSIDPLQARQTYAVGTQHDYFDHDDIIGWTRREGSS 451
Db 361 QGYPSVFGDYGGIPIHGVBSMKSIDPLQARQTYAVGTQHDYFDHDDIIGWTRREGSS 420
Qy 452 HPNSGLATINSDDGGKMMYVGGKAGQVWRDITGNRSGVTITNADGKGFYNGAVS 511
Db 421 HPNSGLATINSDDGGKMMYVGGKAGQVWRDITGNRSGVTITNADGKGFYNGAVS 480
Qy 512 VWVQ 516
Db 481 VWVQ 485

```

RESULT 13
US-10-327-837-1
Sequence 1, Application US/10327837
Publication No. US20030211958A1
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben Vedel
APPLICANT: Bisgaard-Frantzen Henrik
APPLICANT: Oustrup, Helle
APPLICANT: Nielsen, Bjarne Ronfeldt
APPLICANT: Hoeck, Lisbeth Hedegaard
TITLE OF INVENTION: Novel -Amylase And -Amylase Mutants
FILE REFERENCE: 5276.400-US
CURRENT APPLICATION NUMBER: US/10/327,837
CURRENT FILING DATE: 2002-12-23
PRIOR APPLICATION NUMBER: US/09/290,734
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 485
TYPE: PRT
ORGANISM: Bacillus sp.
US-10-327-837-1

Query Match 91.3%; Score 2613; DB 15; Length 485;

Best Local Similarity 95.1%; Pred. No. 9.7e-218;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

```

Qy 32 HHNGTGMQYEFMHLNDGNHNRRLRDDAANKSKGITAVWIPPAKGTSONDVGYGA 91
Db 1 HHNGTGMQYEFMHLNDGNHNRRLRDDAANKSKGITAVWIPPAKGTSONDVGYGA 60
Qy 92 YDLVDLGEFNQKGVRTKYGTRNQLAAVTSLKNGIIOVGDVNMNHKGADGTEIVNAV 151
Db 61 YDLVDLGEFNQKGVRTKYGTRNQLAAVTSLKNGIIOVGDVNMNHKGADGTEIVNAV 120
Qy 152 EVNSNRNOEISGEYTIEMWTKFDFPGKGNTHSNFKRWYHFDGTDMDQSRQLONKIYKF 211
Db 121 EVNSNRNOEISGEYTIEMWTKFDFPGKGNTHSNFKRWYHFDGTDMDQSRQLONKIYKF 180
Qy 212 RGTGKAMDWEVDENGNVDYLMYADVMDHBEVHIELRMGWYNTLTLNDGFRIDA VKH 271
Db 181 RGTGKAMDWEVDENGNVDYLMYADVMDHBEVHIELRMGWYNTLTLNDGFRIDA VKH 240
Qy 272 IKSYTRDMLTHVNTTGGKPMFAVAEFWKNDLAIENYLNKTSWNHSEVDVPLHYNL YNA 331
Db 241 IKSYTRDMLTHVNTTGGKPMFAVAEFWKNDLAIENYLNKTSWNHSEVDVPLHYNL YNA 300
Qy 332 SNSGGEYDMRNILNGSVQKPIHAAVTFVDNHDSQPEALESFYQSWFKPLAVALITRE 391
Db 301 SNSGGEYDMRNILNGSVQKPIHAAVTFVDNHDSQPEALESFYQSWFKPLAVALITRE 360
Qy 392 QGYPSVFGDYGGIPIHGVBSMKSIDPLQARQTYAVGTQHDYFDHDDIIGWTRREGSS 451
Db 361 QGYPSVFGDYGGIPIHGVBSMKSIDPLQARQTYAVGTQHDYFDHDDIIGWTRREGSS 420
Qy 452 HPNSGLATINSDDGGKMMYVGGKAGQVWRDITGNRSGVTITNADGKGFYNGAVS 511
Db 421 HPNSGLATINSDDGGKMMYVGGKAGQVWRDITGNRSGVTITNADGKGFYNGAVS 480
Qy 512 VWVQ 516
Db 481 VWVQ 485

```

RESULT 14
US-10-327-837-7
Sequence 7, Application US/10327837
Publication No. US20030211958A1
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben Vedel
APPLICANT: Bisgaard-Frantzen Henrik
APPLICANT: Oustrup, Helle
APPLICANT: Nielsen, Bjarne Ronfeldt
APPLICANT: Hoeck, Lisbeth Hedegaard
TITLE OF INVENTION: Novel -Amylase And -Amylase Mutants
FILE REFERENCE: 5276.400-US
CURRENT APPLICATION NUMBER: US/10/327,837
CURRENT FILING DATE: 2002-12-23
PRIOR APPLICATION NUMBER: US/09/290,734
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 7
LENGTH: 485
TYPE: PRT
ORGANISM: Bacillus sp.
US-10-327-837-7

Query Match 91.3%; Score 2613; DB 15; Length 485;
Best Local Similarity 95.1%; Pred. No. 9.7e-218;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

```

Qy 32 HHNGTGMQYEFMHLNDGNHNRRLRDDAANKSKGITAVWIPPAKGTSONDVGYGA 91
Db 1 HHNGTGMQYEFMHLNDGNHNRRLRDDAANKSKGITAVWIPPAKGTSONDVGYGA 60

```

```

QY 92 YDLYDLGEFNQKGTVRTKIGTSSQLQAGAVTSLKNNGIQYTGDDVYNNHKGADGTEVNAV 151
DB 61 YDLYDLGEFNQKGTVRTKIGTSSQLQAGAVTSLKNNGIQYTGDDVYNNHKGADGTEVNAV 120
QY 152 EVNRSNRNOETSGEYTAIEAMTKFDPFGKGNTHSNFKRMWYHFDGTDMDOSROLQNKIYKF 211
DB 121 EVNRSNRNOETSGEYTAIEAMTKFDPFGKGNTHSNFKRMWYHFDGTDMDOSROLQNKIYKF 180
QY 212 RGTGKAMDWEVDIENGNDYLYADIMDHPVINELRNMGWYNTNLTLDGFRIDAVKH 271
DB 181 RGTGKAMDWEVDIENGNDYLYADIMDHPVINELRNMGWYNTNLTLDGFRIDAVKH 240
QY 272 IKYSTYRDLTHVRNTTGKMPFAVAFWKNDLAIENYLNKTSNMHSVDPVPLHYNLYNA 331
DB 241 IKYSTYRDLTHVRNTTGKMPFAVAFWKNDLAIENYLNKTSNMHSVDPVPLHYNLYNA 300
QY 332 SNSGGYFDMRNILNGSVVQKHPHIAVTFVNDHDSQGEALSFVQSWFKPLAYALITRE 391
DB 301 SNSGGYFDMRNILNGSVVQKHPHIAVTFVNDHDSQGEALSFVQSWFKPLAYALITRE 360
QY 392 QGYPSVFYGDYGIPTHGVPMSKSIDPLQARQYAYGTQHDYFDHDIIGWTRGDS 451
DB 361 QGYPSVFYGDYGIPTHGVPMSKSIDPLQARQYAYGTQHDYFDHDIIGWTRGDS 420
QY 452 HNSGLATTMSDGPCKMMYVGNKAGQVWRDITGNRSGVTITNADGNGFTVNGAYS 511
DB 421 HNSGLATTMSDGPCKMMYVGNKAGQVWRDITGNRSGVTITNADGNGFTVNGAYS 480
QY 512 VWYKQ 516
DB 481 VWYKQ 485

```

RESULT 15
US-10-665-667-1
; Sequence 1, Application US/10665667
; Publication No. US20040038368A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Miesse, Torben L.
; APPLICANT: Kjaerulf, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/10/665,667
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/769,864
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/183,412
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus
US-10-665-667-1

Query Match 91.3%; Score 2613; DB 15; Length 485;
Best Local Similarity 95.1%; Pred. No. 9.7e-218;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

```

QY 32 HHNGTNGTMMQYFEHMLPNDGNHNRRLRDDAANLKSIGITAWLIPAMKGTSONDVGYGA 91
DB 1 HHNGTNGTMMQYFEHMLPNDGNHNRRLRDDAANLKSIGITAWLIPAMKGTSONDVGYGA 60
QY 92 YDLYDLGEFNQKGTVRTKIGTSSQLQAGAVTSLKNNGIQYTGDDVYNNHKGADGTEVNAV 151
DB 61 YDLYDLGEFNQKGTVRTKIGTSSQLQAGAVTSLKNNGIQYTGDDVYNNHKGADGTEVNAV 120

```

```

QY 152 EVNRSNRNOETSGEYTAIEAMTKFDPFGKGNTHSNFKRMWYHFDGTDMDOSROLQNKIYKF 211
DB 121 EVNRSNRNOETSGEYTAIEAMTKFDPFGKGNTHSNFKRMWYHFDGTDMDOSROLQNKIYKF 180
QY 212 RGTGKAMDWEVDIENGNDYLYADIMDHPVINELRNMGWYNTNLTLDGFRIDAVKH 271
DB 181 RGTGKAMDWEVDIENGNDYLYADIMDHPVINELRNMGWYNTNLTLDGFRIDAVKH 240
QY 272 IKYSTYRDLTHVRNTTGKMPFAVAFWKNDLAIENYLNKTSNMHSVDPVPLHYNLYNA 331
DB 241 IKYSTYRDLTHVRNTTGKMPFAVAFWKNDLAIENYLNKTSNMHSVDPVPLHYNLYNA 300
QY 332 SNSGGYFDMRNILNGSVVQKHPHIAVTFVNDHDSQGEALSFVQSWFKPLAYALITRE 391
DB 301 SNSGGYFDMRNILNGSVVQKHPHIAVTFVNDHDSQGEALSFVQSWFKPLAYALITRE 360
QY 392 QGYPSVFYGDYGIPTHGVPMSKSIDPLQARQYAYGTQHDYFDHDIIGWTRGDS 451
DB 361 QGYPSVFYGDYGIPTHGVPMSKSIDPLQARQYAYGTQHDYFDHDIIGWTRGDS 420
QY 452 HNSGLATTMSDGPCKMMYVGNKAGQVWRDITGNRSGVTITNADGNGFTVNGAYS 511
DB 421 HNSGLATTMSDGPCKMMYVGNKAGQVWRDITGNRSGVTITNADGNGFTVNGAYS 480
QY 512 VWYKQ 516
DB 481 VWYKQ 485

```

Search completed: May 2, 2005, 22:02:08
Job time : 63 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 2, 2005, 21:33:38 ; Search time 23 Seconds

(without alignment)
2158.602 Million cell updates/sec

Title: US-08-952-741-2

Perfect score: 2862

Sequence: 1 MKLHNRIISVLTLLLAVALV.....ADGKGNFTVNGAIVSWVKQ 516

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : PIR 79:*

- 1: PIR1:*
- 2: PIR2:*
- 3: PIR3:*
- 4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2438.5	85.2	518	1 A27705	alpha-amylose (EC
2	1942	67.9	512	1 ALBSL	alpha-amylose (EC
3	1924.5	67.2	549	1 A24541	alpha-amylose (EC
4	1909.5	66.7	549	1 A24549	alpha-amylose (EC
5	1908.5	66.7	549	1 A24436	alpha-amylose (EC
6	1845.5	64.5	514	1 ALBSN	alpha-amylose (EC
7	1837	64.2	548	1 ALBSF	alpha-amylose (EC
8	1347	47.1	493	2 G51713	alpha-amylose (EC
9	1240	43.3	484	2 G5160	alpha-amylose (EC
10	1240	43.3	492	2 AH2079	alpha-amylose (EC
11	1238	43.3	484	2 C86781	alpha-amylose (EC
12	1133	39.6	491	2 G58247	alpha-amylose (EC
13	1090.5	38.1	506	2 G58247	alpha-amylose (EC
14	1084	37.9	495	2 AD3038	alpha-amylose (EC
15	1053	36.8	494	1 B45738	alpha-amylose (EC
16	1045	36.5	494	2 AD0751	alpha-amylose (EC
17	1025	35.8	495	2 B90962	alpha-amylose (EC
18	1022	35.7	495	1 A45738	alpha-amylose (EC
19	1006	35.2	495	2 B85810	alpha-amylose (EC
20	393.5	13.7	217	2 A19506	alpha-amylose (EC
21	323	11.3	1196	2 A29130	beta-amylose (EC 3
22	312.5	10.9	482	2 S31478	alpha-amylose (EC
23	304	10.6	551	2 S05667	glucan 1,4-alpha-m
24	297.5	10.4	440	2 S14958	alpha-amylose (EC
25	295	10.3	421	2 S10514	alpha-amylose (EC
26	287.5	10.0	428	2 T05521	alpha-amylose (EC
27	287	10.0	423	2 T09942	alpha-amylose (EC
28	286.5	10.0	826	2 B96720	probable alpha-amy
29	285	10.0	547	2 A32803	glucan 1,4-alpha-m

30	284.5	9.9	713	2 S09196	cyclomaltoextrin
31	279.5	9.8	438	2 S14957	alpha-amylose (EC
32	278	9.7	713	1 ALBS7	cyclomaltoextrin
33	277	9.7	713	1 ALBS1	cyclomaltoextrin
34	277	9.7	718	1 ALBS3	cyclomaltoextrin
35	275	9.6	712	1 ALBS3	cyclomaltoextrin
36	274.5	9.6	713	2 A58800	cyclomaltoextrin
37	272	9.5	718	1 ALBS6	cyclomaltoextrin
38	270	9.4	528	1 ALBSK	alpha-amylose (EC
39	269.5	9.4	437	2 S14956	alpha-amylose (EC
40	268.5	9.4	435	2 UC7137	alpha-amylose (EC
41	268.5	9.4	438	2 S12625	alpha-amylose (EC
42	268.5	9.4	438	1 ALBH	alpha-amylose (EC
43	267.5	9.3	710	2 S63598	cyclomaltoextrin
44	264	9.2	504	2 A55861	alpha-amylose (EC
45	263.5	9.2	428	2 S10013	alpha-amylose (EC

ALIGNMENTS

RESULT 1
A27705
alpha-amylose (EC 3.2.1.1) precursor - Bacillus sp.
N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase; G6-amyase
C:Species: Bacillus sp.
C:Date: 31-Mar-1989 #sequence_revision 18-Aug-1995 #text_change 16-Aug-2004
C:Accession: A27705
R:Tsukamoto, A.; Kimura, K.; Ishii, Y.; Takano, T.; Yamane, K.
Biochem. Biophys. Res. Commun. 151, 25-31, 1988
A:Title: Nucleotide sequence of the malhexose-producing amyase gene from an alkaloph
A:Reference number: A27705, MUID:88162814, PMID:3258152
A:Accession: A27705
A:Molecule type: DNA
A:Residues: 1-518 <TSU>
A:Cross-references: UNIPROT:P19571; GB:M1862; NID:G142496; PIDN:AAA2231.1; PID:G142497
A:Experimental source: chromosomal DNA of strain 707
A>Note: amino end of mature protein also determined
C:Comment: This is the smallest of five starch-hydrolyzing enzymes from this organism.
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Alpha-amyase, amyloid/faciens type; alpha-amyase, core homology
C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F:1-33/Domain: signal sequence #status predicted <SIG>
F:34-518/Product: alpha-amyase #status experimental <MAT>
F:236-369/Domain: alpha-amyase core homology <AMY>
F:139,238,273/Binding site: calcium (Asn, Asp, His) #status predicted
F:269,299,366/Active site: Asp, Glu, Asp #status predicted
Query Match 85.2%; Score 2438.5; DB 1; Length 518;
Best Local Similarity 83.7%; Pred. No. 3.7e-158;
Matches 426; Conservative 42; Mismatches 40; Indels 1; Gaps 1;
QY 8 ISVLTLLLAVALVFPYMTPEAOAHNGTGMQYEMHLPNGNHNRLRDAANIKS 67
DB 11 LSIILAFLLVLTTS-PTFLVDVEAHNGTGMQYEMHLPNGNHNRLNSDNIKS 69
QY 68 KGITAVWIPPAWKSTQNDVGYGAYDYLDEFPNKGSTVRKTKYGRSOLQGAVTSLKNG 127
DB 70 KGITAVWIPPAWKASQNDVGYGAYDYLDEFPNKGSTVRKTKYGRSOLQGAVTSLKNG 129
QY 128 IQVYGVVNMHKGADGTEVNAVEVRSNRNOEISGEYITAEATKDFPGRGTHSNFK 187
DB 130 IQVYGVVNMHKGADGTEVNAVEVRSNRNOEISGEYITAEATKDFPGRGTHSNFK 189
QY 188 WRWHPDGTMDQROCNKTYKRGTKAMDEYVDLENGYVDLMAADIDMDPEYINE 247
DB 190 WRWHPDGTMDQROCNKTYKRGTKAMDEYVDLENGYVDLMAADIDMDPEYINE 249
QY 248 LRNGVWYNTNLNDGRIDAVKIKYSYTRDWLTHVANTTGKPMFAVEFWKNDLAIIE 307
DB 250 LRNGVWYNTNLNDGRIDAVKIKYSYTRDWLTHVANTTGKPMFAVEFWKNDLAIIE 309

QY 308 NYLNTKSTNHSVDFVPLHNLVNAASNGYFEDMNTLNGSVOKRPHATFVNDHSDQ 367
 A:Accession: 139772
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-32, 'I' <OR>
 A:Cross-references: GB:M62637; NID:G142498; PIDN:AAA2232.1; PID:G142499
 R/Kuhn, H.; Fietzek, P.P.; Lampen, J.O.
 J. Bacteriol. 149, 372-373, 1982
 A:Title: N-terminal amino acid sequence of Bacillus licheniformis alpha-amylase: comparison
 A:Reference number: A26151; MUID:82098050; PMID:6172418
 A:Accession: A26151
 A:Molecule type: protein
 A:Residues: 30-37, 'E', 39-41, 'X', 43-47 <KUH>
 R/Machius, M.; Wiegand, G.; Huber, R.
 J. Mol. Biol. 246, 545-559, 1995
 A:Title: Crystal structure of calcium-depleted Bacillus licheniformis alpha-amylase at 2.
 A:Reference number: S53788; MUID:95182462; PMID:7877175
 A:Accession: S53788
 A:Molecule type: protein
 A:Residues: 'D', 220-227 <MAC>
 A>Note: sequence represents amino end of an internal fragment created by a single enzymat
 R/Machius, M.; Wiegand, G.; Huber, R.
 submitted to the Brookhaven Protein Data Bank, July 1995
 A:Reference number: A65206; PDB:1BPL
 A:Contents: annotation; X-ray crystallography; 2.2 angstroms, residues 32-210; 222-511
 A>Note: these structural studies suggest 163 is Leu rather than Arg
 R/Song, H.K.; Hwang, K.Y.; Chang, C.; Suh, S.W.
 submitted to the Brookhaven Protein Data Bank, October 1996
 A:Reference number: A66860; PDB:1VJ5
 A:Contents: annotation; X-ray crystallography, 1.7 angstroms, residues 32-210; 222-511
 C/Genetics:
 A:Gene: amyL
 C:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C/Superfamily: Alpha-amylase, amylioliquefaciens type; alpha-amylase core homology
 C/Keywords: extracellular protein; glycosylase; heat-stable protein; hydrolase; polysacc
 F:1-29/Domain: signal sequence #status predicted <SID>
 F:30-512/Product: alpha-amylase #status experimental <MNT>
 F:227-360/Domain: alpha-amylase core homology <AMT>
 F:133, 229, 264/Binding site: calcium (Asn, Asp, His) #status experimental
 F:260, 290, 357/Active site: Asp, Glu, Asp #status experimental

RESULT 2
 A:Residues: 1162, 'R', 164-512 <YU>
 A:Cross-references: UNIPROT:P06278; UNIPROT:Q45283; GB:X03236; NID:G39551; PIDN:CAA26981
 A:Experimental source: ATCC 27811
 R/Gray, G.L.; Mainzer, S.E.; Rey, M.W.; Lamasa, M.H.; Kindle, K.L.; Carmona, C.; Requadt,
 J. Bacteriol. 166, 635-643, 1986
 A:Title: Structural genes encoding the thermophilic alpha-amylases of Bacillus stearother
 A:Reference number: A91817; MUID:86195857; PMID:3009417
 A:Accession: A9197
 A:Molecule type: DNA
 A:Residues: 1-338, 'G', 340-348, 'S', 350-512 <GRA>
 A:Residues: 1-338, 'G', 340-348, 'S', 350-512 <GRA>
 A:Cross-references: GB:M13256; NID:G142510; PIDN:AAA2240.1; PID:G142511
 A:Experimental source: NCIB 8061
 R/Stephens, M.A.; Ottlepp, S.A.; Ollington, J.F.; McConnell, D.J.
 J. Bacteriol. 158, 369-372, 1984
 A:Title: Nucleotide sequence of the 5' region of the Bacillus licheniformis alpha-amylase
 A:Reference number: A91796; MUID:84185455; PMID:6609154
 A:Accession: A91796
 A:Molecule type: DNA
 A:Residues: 1-104 <STE>
 A:Cross-references: GB:K01984; NID:G142432; PIDN:AAA22193.1; PID:G142433
 R/Sibakov, M.; Palva, I.
 Eur. J. Biochem. 145, 567-572, 1984
 A:Title: Isolation and the 5'-end nucleotide sequence of Bacillus licheniformis alpha-am
 A:Reference number: A21663; MUID:85076654; PMID:6334606
 A:Accession: A21663
 A:Molecule type: DNA
 A:Residues: 1-3, 'H', 5-12, 'P', 14-47, 'R', 49-61, 'V', 63, 'D', 65-67, 'VA', 70-71, 'S', 73-80, 'D', 8
 A:Experimental source: Chromosomal DNA of ATCC 14580
 A>Note: the authors translated the codon CGT for residue 48 as Gly and GAC for residue 6
 R/Isoide, B.M.; Chambliss, G.H.; McConnell, D.J.
 J. Bacteriol. 171, 2435-2442, 1989
 A:Title: Bacillus licheniformis alpha-amylase gene, amyL, is subject to promoter-independent
 A:Reference number: I39773; MUID:89213924; PMID:2540150
 A:Accession: I39774
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-29 <LMO>
 A:Cross-references: GB:M26412; NID:G341477; PIDN:AAA2237.1; PID:G516590
 R/Orgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Diderichsen, B.
 Gene 96, 37-41, 1990
 A:Title: In vivo genetic engineering: homologous recombination as a tool for plasmid con

A:Reference number: 139772; MUID:91092499; PMID:2265757
 A:Accession: 139772
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-32, 'I' <OR>
 A:Cross-references: GB:M62637; NID:G142498; PIDN:AAA2232.1; PID:G142499
 R/Kuhn, H.; Fietzek, P.P.; Lampen, J.O.
 J. Bacteriol. 149, 372-373, 1982
 A:Title: N-terminal amino acid sequence of Bacillus licheniformis alpha-amylase: comparison
 A:Reference number: A26151; MUID:82098050; PMID:6172418
 A:Accession: A26151
 A:Molecule type: protein
 A:Residues: 30-37, 'E', 39-41, 'X', 43-47 <KUH>
 R/Machius, M.; Wiegand, G.; Huber, R.
 J. Mol. Biol. 246, 545-559, 1995
 A:Title: Crystal structure of calcium-depleted Bacillus licheniformis alpha-amylase at 2.
 A:Reference number: S53788; MUID:95182462; PMID:7877175
 A:Accession: S53788
 A:Molecule type: protein
 A:Residues: 'D', 220-227 <MAC>
 A>Note: sequence represents amino end of an internal fragment created by a single enzymat
 R/Machius, M.; Wiegand, G.; Huber, R.
 submitted to the Brookhaven Protein Data Bank, July 1995
 A:Reference number: A65206; PDB:1BPL
 A:Contents: annotation; X-ray crystallography; 2.2 angstroms, residues 32-210; 222-511
 A>Note: these structural studies suggest 163 is Leu rather than Arg
 R/Song, H.K.; Hwang, K.Y.; Chang, C.; Suh, S.W.
 submitted to the Brookhaven Protein Data Bank, October 1996
 A:Reference number: A66860; PDB:1VJ5
 A:Contents: annotation; X-ray crystallography, 1.7 angstroms, residues 32-210; 222-511
 C/Genetics:
 A:Gene: amyL
 C:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C/Superfamily: Alpha-amylase, amylioliquefaciens type; alpha-amylase core homology
 C/Keywords: extracellular protein; glycosylase; heat-stable protein; hydrolase; polysacc
 F:1-29/Domain: signal sequence #status predicted <SID>
 F:30-512/Product: alpha-amylase #status experimental <MNT>
 F:227-360/Domain: alpha-amylase core homology <AMT>
 F:133, 229, 264/Binding site: calcium (Asn, Asp, His) #status experimental
 F:260, 290, 357/Active site: Asp, Glu, Asp #status experimental

Query Match 67.9%; Score 1942; DB 1; Length 512;
 Best Local Similarity 66.6%; Pred. No. 2e-124;
 Matches 347; Conservative 71; Mismatches 89; Indels 14; Gaps 5;

QY 1 MCLHNRILSVLLTLIAVAVLPPYMTPEQAHHNGTNGTMQYFEWHLPNDGNHNRLED 60
 1 MKQQRKLVARLLTLFLALFLPHSAAAAA-----NLNGTLMQYFEWYMNDDGHWRRQN 56
 DB 1
 QY 61 DAANKSKGITAVWIPPAKGTSONDVCGAYDLVLEFPNQKGYRTKYGTSQIQAV 120
 57 DSAYVLEHGITAVWIPPAKGTSONDVCGAYDLVLEFPNQKGYRTKYGTSQIQAV 116
 DB 121 TSLKXNGIGVGVVWNNHGGADGTEWNAVEVNRNROEISGEYTEAWTKFDPGRG 180
 117 KSLHSDINLVGVVWNNHGGADGTEWNAVEVNRNROEISGEYTEAWTKFDPGRG 176
 DB 181 NTHSNFKWVWYHFDGTDMDQSRQNKIKYFGTGKAMWEDIENGNYDLYMADIDMD 240
 177 STYSDPKWVWYHFDGTDMDQSRQNKIKYFGTGKAMWEDIENGNYDLYMADIDMD 233
 DB 241 HPEVINELRNKGVWYTNLNDGFRIDAVKHKYSTRWLTHTVNTTKKMPFAVAFK 300
 234 HPDVAAEIKRWGIVWYANLEQDGFRLDAVKHKYSTRWLTHTVNTTKKMPFAVAFK 293
 DB 301 NDLAATENTLNTSNHVSFVPLHNLVNAASNGYFEDMNTLNGSVOKRPHATFV 360
 294 NDGALENTLNTSNHVSFVPLHNLVNAASNGYFEDMNTLNGSVOKRPHATFV 353
 DB 361 DNHDSQGEALSFVQSNFKPLAYALILTRGQPSVFGDYGGIPTHG-----VPSMKS 415

Db 354 DNHDTQPGSLESTVQVTEFKPLAVALFILTRESGYPOVFGYDMWG--TKGDSOREIPALKH 411
Qy 416 KIDPLLAQRTAYAGTQHDYFDHDIIGWTRBGSSHPNSGLATIMSDPGKNKMYVQK 475
Db 412 KLEPLKAKQYAYAGTQHDYFDHDIIGWTRBGSSHPNSGLATITDPGSKMYVQK 471
Qy 476 HKAGQWRDITGNRSQVTTINADGNGFTVNGAVSVWV 516
Db 472 QNAGETWHDITGNRSEPVINSEGMGEFVNGSGSVITVQR 512

RESULT 3

A54541
alpha-amylase (EC 3.2.1.1) precursor - *Bacillus stearothermophilus* (strain DN1792)
N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C:Species: *Bacillus stearothermophilus*
C:Date: 28-Oct-1994 #sequence_revision 18-Aug-1995 #text_change 16-Aug-2004
A:Accession: A54541
R:Jorgensen, P. L.; Poulsen, G. B.; Diderichsen, B.
FEMS Microbiol. Lett. 77, 271-276, 1991
A:Title: Cloning of a chromosomal alpha-amylase gene from *Bacillus stearothermophilus*.
A:Reference number: A54541
A:Accession: A54541
A:Molecule type: DNA
A:Residues: 1-549 <J0R>
A:Cross-references: UNIPROT:Q9KMY6; UNIPROT:Q1193; GB:X59476
A:Experimental source: chromosomal DNA of strain DN1792
C:Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
C:Genetics:
A:Start codon: GTG
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Alpha-amylase, amyloliquefactions type; alpha-amylase core homology
C:Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac
F:1-34/Domain: signal sequence #status predicted <SIG>
F:35-549/Product: alpha-amylase #status predicted <MNT>
F:235-368/Domain: alpha-amylase core homology <AMY>
F:113,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
F:266,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 67.2%; Score 1924.5; DB 1; Length 549;
Best Local Similarity 66.0%; Pred. No. 3.4e-123;
Matches 342; Conservative 74; Mismatches 95; Indels 7; Gaps 4;

Qy 1 MCLNRII-----SVLLTLAVALFPYMTBPAQAHNGTGMQYFEMHLPNDGNHN 56
Db 1 MLTFHRIIRKGMWFLALFLVSLFPC-TGQPAKA-AAPFNGTMMQYFEMHLPDGLTMT 58
Qy 57 RLRDDAAMLSKGTITAVIIPAMKGTSONDVGAYDYLDGEFNOGKTVRTKYGTSQ 116
Db 59 KVANEANLSSIGITALLPAPYKGTSDVGAYDYLDGEFNOGKTVRTKYGTSQ 118
Qy 117 QGAVTSLKNGGIQVYGVVNMHKGADGTEWNAVEVRSNRNOISGEYITTEATKDF 176
Db 119 LQALQAAAGQVYADVVPFHKGADGTEWDAVEVPSDRNOISGTYOIQAATKDF 178
Qy 177 FGRGNTSHNFKRWYHFDGTMDOSROLONKIYKRGTKGKAMWEDVLENGYDLYMAD 236
Db 179 FGRGNTSYSPFKRWYHFDGVDMSRKL-SRIYKFRGIGKAMWEDVLENGYDLYMAD 237
Qy 237 IDMHPEVINELRWGVYVTTNLMDGRIDAVHGIKSYTRDWLTHRANTTGKMPAVA 296
Db 238 LDMHPPEVYVTELKMGKRYVTTNIDGRLAVKIKISFPDWLSYRSGTGKPLFTVG 297
Qy 297 EFMKNDLAIENYINKTSWNHSEVDPVLAHNLVYNSNGSGYFDMKNILNGSVQKPTHA 356
Db 298 EYMSWDIKLKNYITKTGTMSLPDAPLHNFYTKSGSGAFDMKRTLTMTILMDQPLA 357
Qy 357 VTFYDNDHDSQGEALIESFVQSMFKPLAVALILITREOGYPSVYGDYGIPTHGVSMSK 416
Db 358 VTFYDNDHDSQGEALIESFVQSMFKPLAVALILITREOGYPSVYGDYGIPTHGVSMSK 417

Qy 417 IDPLLAQRTAYAGTQHDYFDHDIIGWTRBGSSHPNSGLATIMSDPGKNKMYVQK 476
Db 418 IDPLLAQRTAYAGTQHDYFDHDIIGWTRBGSSHPNSGLATITDPGSKMYVQK 477
Qy 477 HKAGQWRDITGNRSQVTTINADGNGFTVNGAVSVWV 514
Db 478 HKAGQWRDITGNRSQVTTINADGNGFTVNGAVSVWV 515

RESULT 4

A24549
alpha-amylase (EC 3.2.1.1) precursor - *Bacillus stearothermophilus* (strain NZ-3)
N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C:Species: *Bacillus stearothermophilus*
C:Date: 30-Jun-1988 #sequence_revision 18-Aug-1995 #text_change 16-Aug-2004
A:Accession: A24549; 139501; 139770
R:Gray, G. L.; Mainzer, S. E.; Rey, M. W.; Lamsa, M. H.; Kindle, K. L.; Carmona, C.; Reguadt,
J. Bacteriol. 166, 635-643, 1986
A:Title: Structural genes encoding the thermophilic alpha-amylases of *Bacillus stearothe*
A:Reference number: A24549
A:Accession: A24549
A:Molecule type: DNA
A:Residues: 1-549 <GRA>
A:Cross-references: GB:M13255; NID:G142512; PIDN:AAA22241.1; PID:G142513
A:Experimental source: genomic DNA of strain NZ-3
R:Satch, H.; Nishida, H.; Isono, K.
J. Bacteriol. 170, 1034-1040, 1988
A:Title: Evidence for movement of the alpha-amylase gene into two phylogenetically dista
A:Reference number: 139501; MUID:86139156; PMID:3257753
A:Accession: 139501
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 536-549 <RES>
A:Cross-references: GB:M29577; NID:G142476; PIDN:AAA22225.1; PID:G142478
A:Experimental source: strain DY-5
A:Accession: 139770
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 536-549 <RE2>
A:Cross-references: GB:M29578; NID:G142484; PIDN:AAA22228.1; PID:G142486
A:Experimental source: strain 799
C:Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
C:Genetics:
A:Start codon: GTG
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Alpha-amylase, amyloliquefactions type; alpha-amylase core homology
C:Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac
F:1-34/Domain: signal sequence #status predicted <SIG>
F:35-549/Product: alpha-amylase #status predicted <MNT>
F:235-368/Domain: alpha-amylase core homology <AMY>
F:113,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
F:266,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 66.7%; Score 1909.5; DB 1; Length 549;
Best Local Similarity 66.0%; Pred. No. 3.5e-122;
Matches 341; Conservative 73; Mismatches 98; Indels 5; Gaps 3;

Qy 1 MCLNRIISVLLTLA---VAVLPYMTBPAQAHNGTGMQYFEMHLPNDGNHN 57
Db 1 MLTFHRIIRKGMWFLALFLVSLFPC-TGQPAKA-AAPFNGTMMQYFEMHLPDGLTMT 59
Qy 58 RLRDDAAMLSKGTITAVIIPAMKGTSONDVGAYDYLDGEFNOGKTVRTKYGTSQ 117
Db 60 VANANLSSIGITALLPAPYKGTSDVGAYDYLDGEFNOGKTVRTKYGTSQ 119
Qy 118 QGAVTSLKNGGIQVYGVVNMHKGADGTEWNAVEVRSNRNOISGEYITTEATKDFP 177
Db 120 QALQAAAGQVYADVVPFHKGADGTEWDAVEVPSDRNOISGTYOIQAATKDFN 179
Qy 178 FGRGNTSHNFKRWYHFDGTMDOSROLONKIYKRGTKGKAMWEDVLENGYDLYMAD 237

DB 180 GRGNTVSFFKRWYHFDGVMDWSRKL-SRIYKFRIGKAMWEDVTENGNDYLMYADL 238

QY 238 DMDHPEVINELRNWGWYNTNTLNDGFRIDAVKHKYSTRDMLTHVRNTTKGPMFAVAE 297

DB 239 DMDHPEVINELRNWGWYNTNTLNDGFRIDAVKHKYSTRDMLTHVRNTTKGPMFAVAE 298

QY 298 FMKNDLALAIENYLNKTSNMHSVFDVPLHYNLNANSGGVFDMRNLINGSVQKPHLHAY 357

DB 299 YMSYDINKLHNYITKTNGTMSLFDAPLHNFYASGSGAFDMSTLNMNTLMKQPTLAV 358

QY 358 TFDVNDHDSOGFALBSFVQSWFKPLAYALILTRGQYPSVFGDYGYGIPTHGVPSMKSXI 417

DB 359 TFDVNDHDSOGFALBSFVQSWFKPLAYALILTRGQYPSVFGDYGYGIPTHGVPSMKSXI 418

QY 418 DPLQARQTYAAYGTOHDYFDHHDIIIGWTRGSDSHSPNSGLATIMSOPGKMKMYGKHK 477

DB 419 DPLQARQTYAAYGTOHDYFDHHDIIIGWTRGSDSHSPNSGLATIMSOPGKMKMYGKHK 478

QY 478 AGQWRDITGNRSQVTITNADGWNFTVNGGAVSVW 514

DB 479 AGQWRDITGNRSQVTITNADGWNFTVNGGAVSVW 515

RESULT 5

A24436

alpha-amyase (EC 3.2.1.1) precursor - Bacillus stearothermophilus plasmid pAT5

N/Alternate names: 1,4-alpha-D-glucan glucanohydrolase

C/Species: Bacillus stearothermophilus

C/Date: 05-Jun-1987 #sequence_revision 18-Aug-1995 #text_change 16-Aug-2004

C/Accession: A24436; I39777

R/Nakajima, R.; Imanaka, T.; Alpa, S.

J. Bacteriol. 163, 401-406, 1985

A/Reference number: A24436; MUID:85234394; PMID:3924897

A/Accession: A24436

A/Molecule type: DNA

A/Residues: 1-549 <NR>

A/Cross-references: UNIPROT:P06279; GB:M1450

A/Experimental source: plasmid pAT5

A/Note: amino end of the mature protein also determined

R/Orgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Diderichsen, B.

Gene 96, 37-41, 1990

A/Title: In vivo genetic engineering: homologous recombination as a tool for plasmid con

A/Reference number: I39772; MUID:91092459; PMID:2265757

A/Accession: I39777

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-45 <RBS>

A/Cross-references: GB:M62638; NID:g142514; PIDN:AAA22242.1; PID:g142515

C/Comment: Alpha-amyase genes have been found on plasmids and in multiple copies on the

C/Genetics:

A/Genes: amyS

A/Genome: plasmid

A/Start codon: GTG

C/Function:

A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A/Pathway: glycogen/starch degradation

C/Superfamily: alpha-amyase, amyloliquefaciens type; alpha-amyase core homology

C/Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac

F/1-34/Domain: signal sequence #status predicted <SIG>

F/35-549/Product: alpha-amyase #status experimental <MAR>

F/335-368/Domain: alpha-amyase core homology <AMY>

F/339, 237, 272/Binding site: calcium (Asp, Asp, His) #status predicted

F/268, 298, 365/Active site: Asp, Glu, Asp #status predicted

Query Match 66.7%; Score 1908.5; DB 1; Length 549;

Best Local Similarity 65.6%; Pred. No. 4.1e-122;

Matches 339; Conservative 75; Mismatches 98; Indels 5; Gaps 3;

QY 1 MKNHNTIS---VLTLLTLLAVAVLFPYMEPBAQHNGNTGTMQYFEWHLPMNDGNHNR 57

DB 1 MTFPHRIIRKGMWFLAFLTLTALLFCPTGQPAKA-APAFNGTMQYFEWHLPMNDGNHNR 59

QY 58 LRDDAANLXSKGTAAVWIPAMKGTSONDVGYADLYDLGEFNQKGTAVTKYGTSSQIQ 117

DB 60 VANEANNLSLIGITLMLPAPAKGTSRSDVGSQVYDLYDLGEFNQKGAARTYGTAKQYL 119

QY 118 GAVTSKKNNGIOYGVYVNMHKGADGTEMVNAVEYNRSNRQETISGETTEAMTKFDP 177

DB 120 QAIQAAHAAGQVYADVVDHDKGADGTEMVNAVEYNRSNRQETISGETTEAMTKFDP 179

QY 178 GRGNTVSFFKRWYHFDGVMDWSRKL-SRIYKFRIGKAMWEDVTENGNDYLMYADL 237

DB 180 GRGNTVSFFKRWYHFDGVMDWSRKL-SRIYKFRIGKAMWEDVTENGNDYLMYADL 238

QY 238 DMDHPEVINELRNWGWYNTNTLNDGFRIDAVKHKYSTRDMLTHVRNTTKGPMFAVAE 297

DB 239 DMDHPEVINELRNWGWYNTNTLNDGFRIDAVKHKYSTRDMLTHVRNTTKGPMFAVAE 298

QY 298 FMKNDLALAIENYLNKTSNMHSVFDVPLHYNLNANSGGVFDMRNLINGSVQKPHLHAY 357

DB 299 YMSYDINKLHNYITKTNGTMSLFDAPLHNFYASGSGAFDMSTLNMNTLMKQPTLAV 358

QY 358 TFDVNDHDSOGFALBSFVQSWFKPLAYALILTRGQYPSVFGDYGYGIPTHGVPSMKSXI 417

DB 359 TFDVNDHDSOGFALBSFVQSWFKPLAYALILTRGQYPSVFGDYGYGIPTHGVPSMKSXI 418

QY 418 DPLQARQTYAAYGTOHDYFDHHDIIIGWTRGSDSHSPNSGLATIMSOPGKMKMYGKHK 477

DB 419 DPLQARQTYAAYGTOHDYFDHHDIIIGWTRGSDSHSPNSGLATIMSOPGKMKMYGKHK 478

QY 478 AGQWRDITGNRSQVTITNADGWNFTVNGGAVSVW 514

DB 479 AGQWRDITGNRSQVTITNADGWNFTVNGGAVSVW 515

RESULT 6

A24436

alpha-amyase (EC 3.2.1.1) precursor - Bacillus amyloliquefaciens

N/Alternate names: 1,4-alpha-D-glucan glucanohydrolase

C/Species: Bacillus amyloliquefaciens

C/Date: 30-Nov-1980 #sequence_revision 30-Jun-1987 #text_change 16-Aug-2004

C/Accession: A92389; A90307; I39756; I39756; A00843

R/Takkinen, K.; Petersson, R.F.; Kalkkinen, N.; Palva, I.; Soderlund, H.; Kaariainen, L.

J. Biol. Chem. 258, 1007-1013, 1983

A/Title: Amino acid sequence of alpha-amyase from Bacillus amyloliquefaciens deduced fr

A/Reference number: A92389; MUID:83108808; PMID:6185474

A/Contents: PUB110

A/Accession: A92389

A/Molecule type: DNA

A/Residues: 1-514 <TRAX>

A/Cross-references: UNIPROT:P00692; GB:J01542; GB:J01543; GB:M12033; GB:M12034; NID:g1424

R/Chung, H.S.; Friedberg, F.

Biochem. J. 185, 387-395, 1980

A/Title: Sequence of the N-terminal half of Bacillus amyloliquefaciens alpha-amyase.

A/Reference number: A90307; MUID:802411725; PMID:6156671

A/Accession: A90307

A/Molecule type: protein

A/Residues: 32-53, 'I', '55-63, 'L', '65-78, 'D', '80-83, 'S', '85-222 <CHU>

R/Palva, I.; Petersson, R.F.; Kalkkinen, N.; Lehtovaara, P.; Sarvas, M.; Soderlund, H.;

Gene 15, 43-51, 1981

A/Title: Nucleotide sequence of the promoter and NH2-terminal signal peptide region of t

A/Reference number: I39756; MUID:82051296; PMID:6170539

A/Accession: I39756

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-96 <RES>

A/Cross-references: EMBL:V00092; NID:g39297; PIDN:CAA23430.1; PID:g39298

R/Ruohonen, L.; Hackman, P.; Lehtovaara, P.; Knowles, J.K.C.; Karanen, S.

Gene 59, 161-170, 1987

A/Title: Efficient secretion of Bacillus amyloliquefaciens alpha-amyase cells by its ow

A/Reference number: I39763; MUID:88137952; PMID:2830166

A/Accession: I39763

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-39 <RES>

A/Cross-references: GB:M18424; NID:g142430; PIDN:AAA22192.1; PID:g142431

C:Function: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycoen/starch degradation
C:Superfamily: Alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F:1-31/Domains: signal sequence #status predicted <SIG>
F:32-514/Product: alpha-amylase #status predicted <MPT>
F:129-362/Domains: alpha-amylase core homology <AMY>
F:133,231,266/Binding site: calcium (Asn, Asp, His) #status predicted
F:262,292,359/Active site: Asp, Glu, Asp #status predicted

Query Match 64.5%; Score 1845.5; DB 1; Length 514;
Best Local Similarity 63.8%; Pred. No. 7.2e-118;
Matches 329; Conservative 74; Mismatches 100; Indels 13; Gaps 4;

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QY 6 RIISLTLTLLAVLFPYMTPEPAQHNGTNGTMMQYFEMHLIPNDGNHMRRLDADAHL 65
DB 7 RIVSRRLVLMCTLFLVSPIDTKT---SAVNGTLMQYFEMHTPNDGQHWKRLDADAHL 61
QY 66 KSKGTTAVWIPPAWKGTSQNDVGYGAYDYLDFEFNQGTVTRTKYTSQIGATSLIKN 125
DB 62 SDIGTTAVWIPPAWKGTSQNDVGYGAYDYLDFEFNQGTVTRTKYTSQIGATSLIKN 121
QY 126 NGIYGVGVNHHKGGADGTEWVNAVEVNSNRNOISGEYTTIEMTKYFDPFGNGTSHN 185
DB 122 RNVQYGVGVNHHKGGADGTEWVNAVEVNSNRNOISGEYTTIEMTKYFDPFGNGTSHN 181
QY 186 FKMWHYHEDGTPDMSROLOKIKYKRGTKAMPEDVNIENGNYDLYMAYADIMDHEVI 245
DB 182 FKMWHYHEDGTPDMSROLOKIKYKRGTKAMPEDVNIENGNYDLYMAYADIMDHEVI 240
QY 246 NELNMGVWYNTNLNDGFRIDAVGHIKYSYTRDMLTAVRTTQKPMFAVAFKMDLAA 305
DB 241 AETKMGWYANELSLDFRIDAAGHIKFSFLRDMVQAVRQATGEMTVAEYQNNKNG 300
QY 306 IENTYKTSWNSVFDVPLHYNLYNASNGYFDMENILNGSVYQKPIHATVPNDHS 365
DB 301 LENTYKTSWNSVFDVPLHYNLYNASNGYFDMENILNGSVYQKPIHATVPNDHS 360
QY 366 QPGEALSFVQSWKPELAVALLITREOGYPSVFYGDYGIPTHG-----VSMKSKIDPL 420
DB 361 QPGEALSFVQSWKPELAVALLITREOGYPSVFYGDYGIPTHG-----VSMKSKIDPL 418
QY 421 LQAGQYAVYGTQHDYFDHDIIGWTRREGDSHPNSGLATIMSDGPGKMMYVYGKHAQ 480
DB 419 LKAKRYAVYGTQHDYFDHDIIGWTRREGDSHPNSGLATIMSDGPGKMMYVYGKHAQ 478
QY 481 VWRDITGNRSGTITINDGWNFTVNGAVSWYKQ 516
DB 479 TWYDITGNRSGTITINDGWNFTVNGAVSWYKQ 514
```

RESULT 7

ALBSP
alpha-amylase (EC 3.2.1.1) precursor - *Bacillus stearothermophilus* (strain DY-5) plasmid

N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C:Species: *Bacillus stearothermophilus*
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Aug-2004

C:Accession: A91999; B91999; A00845
R:Inara, H.; Sasaki, T.; Tsuboi, A.; Yamagata, H.; Tsukagoshi, N.; Uda, S.

J. Biochem. 98, 95-103, 1985
A:Title: Complete nucleotide sequence of a thermophilic alpha-amylase gene: homology bet

A:Reference number: A91999; MUID:86008166; PMID:3876333
A:Accession: A91999

A:Molecule type: DNA
A:Residues: 1-548 <1H1>

A:Cross-references: UNIPROT:P06279; GB:X02769
A:Experimental source: plasmid pHI300 from strain DY-5

A:Accession: B91999
A:Molecule type: protein

A:Residues: 35-48 <1H2>
A:Experimental source: strain DY-5

R:Tsukagoshi, N.; Iritani, S.; Sasaki, T.; Takemura, T.; Ihara, H.; Idota, Y.; Yamagata,

J. Bacteriol. 164, 1182-1187, 1985
A:Title: Efficient synthesis and secretion of a thermophilic alpha-amylase by protein-pr

A:Reference number: A91804; MUID:86059211; PMID:2999073
A:Contents: pBAM101

A:Accession: A91804
A:Molecule type: DNA

A:Residues: 1-29, 'Q', 31-75, 'W', 77-122 <TSU>
A:Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the

C:Genetics:
A:Genome: plasmid

A:Start codon: GTG
C:Function: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycoen/starch degradation

C:Superfamily: Alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C:Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac

F:1-34/Domains: signal sequence #status predicted <SIG>
F:35-548/Product: alpha-amylase #status experimental <MAT>
F:129-368/Domains: alpha-amylase core homology <AMY>
F:133,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
F:268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 64.2%; Score 1837; DB 1; Length 548;
Best Local Similarity 63.7%; Pred. No. 3e-117;
Matches 331; Conservative 71; Mismatches 106; Indels 12; Gaps 5;

```
QY 1 MKNHRIIS---VLTLLLAVALFPYMTPEPAQHNGT---NGTMMQYFEMHLIPNDGNH 54
DB 1 MKNHRIIS---VLTLLLAVALFPYMTPEPAQHNGT---NGTMMQYFEMHLIPNDGNH 56
QY 55 WNRRLDAAANLKSIGITAWIPPAWKGTSQNDVGYGAYDYLDFEFNQGTVTRTKYTSQ 114
DB 57 WTKYANENNLSSIGITAWIPPAWKGTSQNDVGYGAYDYLDFEFNQGTVTRTKYTSQ 116
QY 115 QLGAVTSLKNGIGIYGVGVNHHKGGADGTEWVNAVEVNSNRNOISGEYTTIEMTKY 174
DB 117 QYLGAVTSLKNGIGIYGVGVNHHKGGADGTEWVNAVEVNSNRNOISGEYTTIEMTKY 176
QY 175 DFGNGTSHNSFKRWYHFDGTPDMSROLOKIKYKRGTKAMPEDVNIENGNYDLYMAY 234
DB 177 DFGNGTSHNSFKRWYHFDGTPDMSROLOKIKYKRGTKAMPEDVNIENGNYDLYMAY 235
QY 235 ADIMDHEVNIENLKNMGVWYNTNLNDGFRIDAVGHIKYSYTRDMLTAVRTTQKPMFA 294
DB 236 ADIMDHEVNIENLKNMGVWYNTNLNDGFRIDAVGHIKYSYTRDMLTAVRTTQKPMFA 295
QY 295 VAEFWKNDLAIENYLNKTSWNSVFDVPLHYNLYNASNGYFDMENILNGSVYQKPI 354
DB 296 VAEFWKNDLAIENYLNKTSWNSVFDVPLHYNLYNASNGYFDMENILNGSVYQKPI 355
QY 355 HATVFNHDSQPEALSFVQSWKPELAVALLITREOGYPSVFYGDYGIPTHGSMK 414
DB 356 HATVFNHDSQPEALSFVQSWKPELAVALLITREOGYPSVFYGDYGIPTHGSMK 414
QY 415 SKIDPLQAGQYAVYGTQHDYFDHDIIGWTRREGDSHPNSGLATIMSDGPGKMMYVYG 474
DB 415 SKIDPLQAGQYAVYGTQHDYFDHDIIGWTRREGDSHPNSGLATIMSDGPGKMMYVYG 474
QY 475 KHAQYVWRDITGNRSGTITINDGWNFTVNGAVSWYKQ 514
DB 475 KHAQYVWRDITGNRSGTITINDGWNFTVNGAVSWYKQ 514
```

RESULT 8

alpha-amylase (EC 3.2.1.1) - *Bacillus circulans*

C:Species: *Bacillus circulans*
C:Date: 18-Feb-1984 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C:Accession: S15713
R:Marcel, T.

submitted to the EMBL Data Library, May 1991
A:Reference number: S15713

A:Accession: S15713

A:Molecule type: DNA
 A:Residues: 1-493 <MAR>
 A:Cross-references: UNIPROT:Q03657; EMBL:X60779; NID:g39411; PIDN:CAA3194.1; PID:g39412
 C:Genetics:
 A:Gene: amyE
 C:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: alpha-amyase, amyloliquefaciens type; alpha-amyase core homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:200-333/Domains: alpha-amyase core homology <AMY>

Query Match 47.1%; Score 1347; DB 2; Length 493;
 Best Local Similarity 51.4%; Pred. No. 5.1e-84;
 Matches 247; Conservative 73; Mismatches 153; Indels 8; Gaps 3;

```

QY 37 NGTMMQYFEFHHLPNDGNHNRRLRDAANLKSIGITAWIPPAWKGTSQNDVGYGAYDLYD 96
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 4 NHTMMQFEFHHLPNDGNHNRRLRDAANLKSIGITAWIPPAWKGTSQNDVGYGAYDLYD 63
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 97 LGSEFNQKGVTRTKYKGTGRSOLQAVTSLKNNGIQYGVVNNHKGADGTEMNAVEVNR 156
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 64 LGSEFNQKGVTRTKYKGTGRSOLQAVTSLKNNGIQYGVVNNHKGADGTEMNAVEVNR 123
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 157 NNRQETSGEYTTIEMTKFPPGKGNTHSNFKMRWYHFDGTDMDQSRLOKIKYKPGTGK 216
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 124 DRKTEISEPPELIGMTKFTPGRGDOYSFKMNSHHNGTDPD-AREERTGVRIAGENK 182
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 217 AMDMEVDIENGNDYLYMAYADIDMDHPEVINELRNWGVYNTNTLNDGFRIDAVKHIKYSY 276
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 183 KMNENVDDEFNGVDYLMFAIDYVNHDPVREMIIDMGKMLDITLQCGGFRIDALIKHINHEF 242
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 277 TRDMLTHVRNTTGKPMFAVAEPKNDLALIENTLNTKSNHSHFDDVPLHNLVYNAISG 336
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 243 IKFAEMIKRQODFYIYVEFPMNSNLDACREFLDTYQIDLPDYLAKHKAHSLKGR 302
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 337 YFMRNLINGSVQKHPHIAVTFDNHDSDGSEALSEFVQSWKPLAYALLITREOGYPS 396
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 303 DPLDKIFDITVOTHTHVAITFDVNDHSDPHRLBSWIDMKRPSYALLTLRRDQY 362
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 397 VFYGDYGGI----PTHGVPMSKSIDPLLOARQYAYGTQHDYFDHHDIIIGWTREDSH 452
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 363 VFYGDYGGI--GPEPVDG---KKEILDITLISARCNKAGGEDEYFDHANTIGWRGVEEI 419
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 453 PMSGGLATIMDGGKGNMVTYVGHKAGQVARDITGNRSGVTINADGWFYNGAVSY 512
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 420 EGSGCAVVISGNDGKRMFIDGEHAGEVWVDLTKSCDQITIEDGMATFHVCGGGSV 479
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 513 W 513
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 480 W 480
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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RESULT 9

alpha-amyase [imported] - Streptococcus pneumoniae (strain TIGR4)
 C:Species: Streptococcus pneumoniae
 C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
 C:Accession: G95160
 R:Retelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
 on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzaple,
 nson, T.; Hickey, E.K.; Holt, I.E.
 Science 293, 498-506, 2001
 A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
 A.; Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
 A:Reference number: A95000; MUID:21357209; PMID:11463916
 A:Accession: G95160
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-484 <KOR>
 A:Cross-references: UNIPROT:Q97049; GB:AE005672; PIDN:AAK75480.1; PID:g14972868; GSPDB:C
 A:Experimental source: strain TIGR4
 C:Genetics:

A:Gene: SPI382
 C:Superfamily: alpha-amyase, amyloliquefaciens type; alpha-amyase core homology
 Query Match 43.3%; Score 1240; DB 2; Length 484;
 Best Local Similarity 48.8%; Pred. No. 9.4e-77;
 Matches 234; Conservative 74; Mismatches 166; Indels 6; Gaps 4;

```

QY 37 NGTMMQYFEFHHLPNDGNHNRRLRDAANLKSIGITAWIPPAWKGTSQNDVGYGAYDLYD 96
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 NHTMMQFEFHHLPNDGNHNRRLRDAANLKSIGITAWIPPAWKGTSQNDVGYGAYDLYD 62
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 97 LGSEFNQKGVTRTKYKGTGRSOLQAVTSLKNNGIQYGVVNNHKGADGTEMNAVEVNR 156
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 LGSEFNQKGVTRTKYKGTGRSOLQAVTSLKNNGIQYGVVNNHKGADGTEMNAVEVNR 122
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 157 NNRQETSGEYTTIEMTKFPPGKGNTHSNFKMRWYHFDGTDMDQSRLOKIKYKPGTGK 216
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 123 DRTELGESEFTINGWTSFFDGRDQTYNGFHHWHFTGTDYDARKS-KSGITLQGDYK 181
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 217 AMDME--VDIENGNDYLYMAYADIDMDHPEVINELRNWGVYNTNTLNDGFRIDAVKHIKYSY 274
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 182 GWANBELVNDENGNDYLYMAYADIDMDHPEVINELRNWGVYNTNTLNDGFRIDAVKHIKYSY 241
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 275 SYTRDMLTHVRNTTGKPMFAVAEPKNDLALIENTLNTKSNHSHFDDVPLHNLVYNAISG 334
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 242 FFMENRIFRMKKEKYGDDFVFGSEFNNPDKEANLIDLEKTEEHFDLYDVRHLQNLFEASQA 301
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 335 GGYFDMKRLINGSVQKHPHIAVTFDNHDSDGSEALSEFVQSWKPLAYALLITREOGY 394
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 302 GANYDLRGIFFTSLVELKDKKAVTFPDNHDYTGQALSTVEWEPFAVYALLITRKQDEL 361
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 395 PSYFVGDDYGIIP-THGVPMSKSIDPLLOARQYAYGTQHDYFDHHDIIIGWTREDSH 453
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 362 PCVFYDYGIGISQVYAOEPKELIDRLAIRKDLYAGEONDYFDHANCIGWRSG--AAN 419
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 454 NSGLATIMDGGKGNMVTYVGHKAGQVARDITGNRSGVTINADGWFYNGAVSY 513
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 420 QSPIAVLISNDQNSKSMFVGQEWNTQTFVDLGNHQQGVITIDEGYQFPVSARSVS 479
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

RESULT 10

alpha-amyase [imported] - Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp. PCC 7120
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 16-Aug-2004
 C:Accession: AH2079
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anat
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AH2079
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-492 <KOR>
 A:Cross-references: UNIPROT:Q8YU21; GB:BA000019; PIDN:BAW73689.1; PID:g17131281; GSPDB:G
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Superfamily: Alpha-amyase, amyloliquefaciens type; alpha-amyase core homology

Query Match 43.3%; Score 1240; DB 2; Length 492;
 Best Local Similarity 48.4%; Pred. No. 9.6e-77;
 Matches 228; Conservative 79; Mismatches 157; Indels 18; Gaps 6;

```

QY 37 NGTMMQYFEFHHLPNDGNHNRRLRDAANLKSIGITAWIPPAWKGTSQNDVGYGAYDLY 95
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 5 NHTMMQYFEFHHLPNDGNHNRRLRDAANLKSIGITAWIPPAWKGTSQNDVGYGAYDLY 64
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 96 DLGEFNQKGVTRTKYKGTGRSOLQAVTSLKNNGIQYGVVNNHKGADGTEMNAVEVNR 155
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 65 DLGEFNQKGVTRTKYKGTGRSOLQAVTSLKNNGIQYGVVNNHKGADGTEMNAVEVNR 124
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```


RESULT 13

G98247

Cyttoplasmic alpha-amylase (1,4-alpha-D-glucan glucanohydrolase) [Imported] - Agrobacterium tumefaciens

C/Species: Agrobacterium tumefaciens

C/Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004

C/Accession: G98247

R/Gooder, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quirio, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markels, B.

Science 294, 2323-2328, 2001

A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens

A/Reference number: A97559; MUID:21608551; PMID:11743194

A/Accession: G98247

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-506 <KUR>

A/Cross-references: UNIPROT:Q8U916; GB:AE007870; PID:AAK89505.1; PID:g15159379; GSPDB:C

A/Gene: AGR_1863

A/Map position: linear chromosome

C/Superfamily: alpha-amylase, amy101quefaciens type; alpha-amylase core homology

Query Match 38.1%; Score 1090.5; DB 2; Length 506;

Best Local Similarity 44.3%; Pred. No. 1.4e-66;

Matches 224; Conservative 80; Mismatches 181; Indels 21; Gaps 9;

25 MTEPAQAHNG--TNGTMOYFEWHL.PNDGNHNRRLDDAANKSKGITAVMIPPAWKGT 82

1 MARPAN-HREGNMAGRITLQFFHWYDPDGGKLMSEVAEKLAKMGITDVMLEPPAYKGA 59

83 SQN-DVGYGAYDLYDLGFENQKGTNRKTKYGRSLOQAVSLKNGIQYGVGVVMMHKGK 141

60 AGGVSQYDYDLYDLGFENQKGTNRKTKYGRSLOQAVSLKNGIQYGVGVVMMHKGK 119

142 ADGTEWNAEVAEVRNSNRNOELSGEYTEATKEDPFGKGNTHSNFKRWYHFDGTWDS 201

120 ADEKRAKRVARVNDPDDTDIDDEPRLATYRFFPRNKGHSFIMDLKCFSGVDHIE- 178

202 ROLNKKYKF--RGTSKAMDEVDIENGNYDYLMVADIMDHPEVINEIRNMGWYTTNT 258

179 EPTEDGIFRLVNEYGDE--WNEEVDQENGFEDYLMGADVEFRNPAVVEELKYGWMLSEQ 237

259 LINDGFRIDAVKHIKYSYTDWMLTHVNTTGKMPFAAEFKNDLAIENTYLNKTSWNHS 318

238 VQVDFGLDAKHI.PANFPRDWGMRKETYDPLFLVALEYTHNPDELYKYLDELVDKQLM 297

319 VFDPVLYNLYNANSGYFPMRNILNGSVVQKAPHAVTFVDNHSQPEALSFVQSN 378

298 LFDVALHHSFHDASKOGGDFMRSIFDGSLSAVPDAVTLVDNHTQPLQSLAPVEPW 357

379 FKPLAYALILTRGQYGVFYGYDYG--IPTHGVPSMKSKID-----PLQARQTYA 428

358 FKPLAYALILTRGQYGVFYGYDYG--IPTHGVPSMKSKID-----PLQARQTYA 417

429 YGTQHDVFDHDDIIGMTREDSHPNSGLATIMSDGPGNKMVYGGKXAGQVWRDITGN 488

418 NGPOTDIFDDASCTAFIRHGTADAP--GCVVVMNSNGEPEKQADLGPBRAGSVWRDILGH 475

489 RSGVTITNADGMGNTVNGAVSVWV 514

476 REEHITLDESCKGFFPTNGSGSVSWV 501

RESULT 14

alpha-amylase amya [Imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C/Species: Agrobacterium tumefaciens

C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 16-Aug-2004

C/Accession: AD3038

R/Mood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell

Science 294, 2317-2323, 2001

A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, J.

A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A/Reference number: A42577; MUID:21608550; PMID:11743193

A/Accession: AD3038

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-495 <KUR>

A/Cross-references: UNIPROT:Q8U916; GB:AE008689; PID:AA44722.1; PID:g17742354; GSPDB:G

A/Experimental source: strain C58 (Dupont)

A/Genetics:

A/Map position: linear chromosome

C/Superfamily: Alpha-amylase, amy101quefaciens type; alpha-amylase core homology

Query Match 37.9%; Score 1084; DB 2; Length 495;

Best Local Similarity 44.7%; Pred. No. 3.9e-66;

Matches 219; Conservative 80; Mismatches 173; Indels 18; Gaps 7;

39 TMQYFEWHL.PNDGNHNRRLDDAANKSKGITAVMIPPAWKGTSON-DVGYGAYDLYDL 97

5 TLLQFFHWYDPDGGKLMSEVAEKLAKMGITDVMLEPPAYKGAAGYSVGYDLYDL 64

98 GFENQKGTNRKTKYGRSLOQAVSLKNGIQYGVGVVMMHKGADGTEWNAEVRNSN 157

65 GFEDQKGTAVATKGRALAEHAGKTLKONGIRVHIDVNLHMGADKEKAVRREVPD 124

158 KNOELSGEYTEATKEDPFGKGNTHSNFKRWYHFDGTWDSQOLNKKYKF--RGT 214

125 RTDIDEDPRLATYRFFPRNKGHSFIMDLKCFSGVDHIE-EPTEDGIFRLVNEYG 183

215 GRAMDEVDIENGNYDYLMVADIMDHPEVINEIRNMGWYTTNTLNGFRIDAVKHIKY 274

184 GE-WNEEVDQENGFEDYLMGADVEFRNPAVVEELKYGWMLSEQVQVDFGLDAKHI 242

275 SYTRDWLTHVNTTGKMPFAAEFKNDLAIENTYLNKTSWNHSVFDVPLHYNLYNANS 334

243 WFRDWGMRKETYDPLFLVALEYTHNPDELYKYLDELVDKQLMFLDVALHHSFHDASKO 302

335 GGYFPMRNILNGSVVQKAPHAVTFVDNHSQPEALSFVQSNFKPLAYALILTRGQY 394

303 GGFPMRSIFDGSLSAVPDAVTLVDNHTQPLQSLAPVEPWFKPLAYALILTRGQY 362

395 PSVFGDYDYG--IPTHGVPSMKSKID-----PLQARQTYAVGTQHDVFDHDDIGW 444

363 PCYFYDLEGTSTDTGNGNEKIDIPALIECLPKLIEARSPANGPQDIFDDASCTAF 422

445 TREGDSHPNSGLATIMSDGPGNKMVYGGKXAGQVWRDITGNNGVTITNADGMGNT 504

423 IRHGTADAP--GCVVVMNSNGEPEKQADLGPBRAGSVWRDILGHREHITLDESCKGTFP 480

505 VNGGAVSVWV 514

481 TNGGAVSVWV 490

RESULT 15

alpha-amylase (EC 3.2.1.1), cytosolic - Salmonella typhimurium

N/Alternate names: 1,4-alpha-D-glucan glucanohydrolase

C/Species: Salmonella typhimurium

C/Date: 07-Apr-1994 #sequence_revision 18-Aug-1995 #text_change 16-Aug-2004

C/Accession: B45738

R/Raha, M.; Kawagishi, I.; Mueller, V.; Kihara, M.; Macnab, R.M.

J. Bacteriol. 174, 6644-6652, 1992

A/Title: Escherichia coli produces a cytoplasmic alpha-amylase, amyaA.

A/Reference number: A45738; MUID:93015717; PMID:1400215

A/Accession: B45738

A/Molecule type: DNA

A/Residues: 1-494 <RAN>

A/Cross-references: UNIPROT:P26613; GB:L01643; NID:g154043; PID:AAA27110.1; PID:g154045

C/Genetics:

A/Gene: amya

C;Function:

A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation

A; Pathway: glycogen/starch degradation

C:Superfamily: alpha-amylase, amylioliquefaciens type, alpha-amylase core homology
C:Keywords: cytosol; glycosidase; hydrolase; polysaccharide degradation

Keywords: cytosol; glycosidase; hydrolase; polysaccharide degradation

F;202-335/Domain: alpha-amylase core homology <AMY>
F;239,265,332/Active site: His, Glu, Asp #status predicted

F:239,265,332/Active site: His, Glu, Asp #status predicted

Query Match	36.8%;	Score 1053;	DB.1;	Length 494;
Best Local Similarity	42.1%;	Pred. No. 4.9e-64;		
Matches 207;	Conservative	84;	Mismatches 183;	Indels 18;
				Gaps 6;

```

0Y 37 IGTMAQYEPFMI,PNJCNHNHNR,LRDDAAN,KSXKITAVMI,PPAKGNSQN--DYVQGAVDLY 95
Db 3 NPTLIQYFHWYIPDGGKLMSELAERADGINDGINMWLPEACKGASGGYSVGDITDYL 62
0Y DLGEFNOKGTATYTKYSTRSLOGAVSLKNNGIQVYGDVVMNKGADGTEMNAVEVR 155
Db 63 DLGEFDQKGTITKTKGDKRQLTALDALKKNNIAVLDDVVMNKGADDEKERIRVQRVNO 122
0Y 156 SNRNOEISGEYTI,EAWTKFPD,PGRGNTHSNFKRWYHFDGTDWDSROLONKIYKRG-- 213
Db 123 DDRQTIDNNIIRCEGWTRYTPFPBAQOYSNFIWDYHCFSGIDHIEHPD--EDGIFKLVNDY 181
0Y 214 TGKAMDWEYDINGNVYD,MTADIDMDHEVINE,LNKGWYVNTYNTLNDGFRIDAVKHIK 273
Db 182 TGDGNNDQDDVMDEGNFDYLMGSEINDFERNHAAVTEIEIKYMARWVEQTHCGFRIDAVGHIR 241
0Y 274 YSYTRDMLTHVANTTGKPMFAVAEFMKNDLAI,ENLTAKTSMNHSFDPVRHLNLYASN 333
Db 242 AMEYEWEMIEHVOAVALPKPLFAEYVSHVEDKIQTYIDVDGKTM,FDP,LOMKFHEASR 301
0Y 334 SGGYFDMENI,INLNGSVOKRPIHAFTFVDNHDSDSGEALESPVOGMEFKPLATYALITREOG 393
Db 302 OGAEVDMGHI,FGTGLVEADPFPAVTLVANHDPDPLDALRPAVPMFKPLATYALITLRENG 361
0Y 394 YPSVFEYDYGIPTH-----GVBSMKSKIDPRLQARQTYAVGTOHDFDHHDI 442
Db 362 VPSVFYRPLDYGASVEDSGENGECRVDMELV--NQDLRLILARQFPAHGQITLRFPHDNCI 420
0Y 443 GWTRGCDSDHPHSGLATIMSDBGKKNMYVGKHKAGQVWRDITGNRSGVTITNADGMGN 502
Db 421 AFSRSGTEENP--GCVVYVLSNGDDGEKTLILDGNYANKTWDRPFSGNRDEYVVTNDGGEAT 478
0Y 503 FTVNGGAVSVMY 514
Db 479 PFCNAGSVSMY 490

```

Search completed: May 2, 2005, 21:56:41
Job time : 25 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 2, 2005, 20:14:23 ; Search time 73 Seconds

(without alignments)
3619.628 Million cell updates/sec

Title: US-08-952-741-2

Perfect score: 2862
Sequence: 1 MKLHNRIISVLTLLAVAV.....ADGKGNFTVGNAGNVAVKQ 516Scoring table: BIOSUM62
Gap 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summariesDatabase : Uniprot 03:.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2862	100.0	516	2	082839 bacillus sp
2	2438.5	85.2	518	1	AMT6_BACS7
3	1958.5	68.4	613	2	Q59222
4	1957.5	68.4	513	2	Q81AS4
5	1957.5	68.4	533	2	Q9A054
6	1952.5	68.2	513	2	Q81YJ4
7	1948.5	68.1	513	2	Q6HPU3
8	1942	67.9	512	1	AMY_BACLI
9	1936	67.6	512	2	Q65MX0
10	1923.5	67.2	519	2	Q9R0T8
11	1915.5	66.9	521	2	P71034
12	1915.5	66.9	549	2	Q9KWF6
13	1913.5	66.9	549	2	Q31193
14	1908.5	66.7	549	1	AMY_BACST
15	1866	65.2	501	2	Q93148
16	1845.5	64.5	514	1	AMY_BACAM
17	1560.5	54.5	507	2	Q87HG6
18	1347	47.1	493	2	Q03657
19	1337	46.7	481	2	Q89VPI
20	1329	46.4	481	2	Q64RC7
21	1276.5	44.6	486	2	Q8DT08
22	1270.5	44.4	488	2	Q8E0M2
23	1267.5	44.3	488	2	Q8E696
24	1240	43.3	484	2	Q97049
25	1240	43.3	492	2	Q8YU21
26	1238	43.3	484	2	Q8DPC8
27	1237.5	43.2	486	2	Q88875
28	1223.5	42.7	484	2	Q50583
29	1204.5	42.1	485	2	Q53786
30	1133	39.6	491	2	Q9CG59
31	1090.5	38.1	506	2	Q7CTI9

32	1084	37.9	495	2	Q8U916	Q8U916 agrobacteri
33	1075	37.6	539	2	Q6MMW6	Q6MMW6 neurospora
34	1051	36.7	494	1	AMY2_SALTY	P26613 salmonella
35	1048	36.6	531	2	Q7SEB7	Q7SEB7 neurospora
36	1045	36.5	494	2	Q8Z5B5	Q8Z5B5 salmonella
37	1027	35.9	495	2	Q8FGI8	Q8FGI8 escherichia
38	1025	35.8	495	2	Q7AD04	P26612 escherichia
39	1022	35.7	495	1	AMY2_ECOLI	Q7AD04 escherichia
40	1020	35.6	495	2	Q7UAB0	Q7UAB0 shigella fl
41	1018	35.6	495	2	Q83R40	Q83R40 shigella fl
42	1006	35.2	495	2	Q8XBB6	Q8XBB6 escherichia
43	999.5	34.9	529	2	Q877B1	Q877B1 aspergillus
44	928	32.4	654	2	Q7SS35	Q7SS35 neurospora
45	760	26.6	587	2	Q6WUB6	Q6WUB6 alkaliphil

ALIGNMENTS

RESULT 1					
ID	082839	PRELIMINARY;	PRT;	516 AA.	
AC	082839;				
DT	01-NOV-1998 (TREMblrel. 08, Created)				
DT	01-NOV-1998 (TREMblrel. 08, Last sequence update)				
DT	01-JUN-2003 (TREMblrel. 24, Last annotation update)				
DE	Amylase.				
OS	Bacillus sp.				
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.				
OX	NCBI_TaxID=1409;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=KSM-1378;				
RX	MEDLINE=96342096; PubMed=9675143; DOI=10.1006/dbrc.1998.8970;				
RA	Igarashi K., Hatada Y., Ikawa K., Araki H., Ozawa T., Kobayashi T.,				
RA	Ozaki K., Ito S.;				
RT	"Improved thermostability of a Bacillus alpha-amylase by deletion of				
RT	an arginine-glycine residue is caused by enhanced calcium binding.";				
RL	Biochem. Biophys. Res. Commun. 248:372-377(1998).				
CC	-I-SIMILARITY: Belongs to family 13 of glycosyl hydrolases.				
DR	EMBL; AB008763; BAA32431.1; -				
DR	HSSP; P06278; IVUS.				
DR	GO; GO:0004556; F:alpha-amylase activity; IEA.				
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.				
DR	InterPro; IPR006047; Alpha_amyl_cat.				
DR	InterPro; IPR006589; Alp_amyl_cat_sub.				
DR	InterPro; IPR006046; Glyco_hydro_13.				
DR	Pfam; PF00128; Alpha-amylase; 1.				
DR	PRINTS; PR00110; ALPHAMYLASE.				
DR	SMART; SM00642; Amy; 1.				
DR	SEQUENCE 516 AA; 58841 MW; D90ABCG0ECC182F8 CRC64;				
Query Match 100.0%; Score 2862; DB 2; Length 516;					
Best Local Similarity 100.0%; Pred. No. 6, 9e-185;					
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1	MKLHNRIISVLTLLAVAVLPYPTPEPAQHNGNTGTMQYFEWHLNDGNTFNRIRD	60		
Db	1	MKLHNRIISVLTLLAVAVLPYPTPEPAQHNGNTGTMQYFEWHLNDGNTFNRIRD	60		
Qy	61	DAANLKSRTAIVIPRAWKGTSNDVYGAYDLYDGEPFOKGTATKGTGTRSLQGV	120		
Db	61	DAANLKSRTAIVIPRAWKGTSNDVYGAYDLYDGEPFOKGTATKGTGTRSLQGV	120		
Qy	121	TSLKNGIGIYVGDVVMHKGAGDTENVNAVEVNRNRNOEISGEYTIKATKDFPGR	180		
Db	121	TSLKNGIGIYVGDVVMHKGAGDTENVNAVEVNRNRNOEISGEYTIKATKDFPGR	180		
Qy	181	NTSHNFKRWYHFDGTDWDSROLQNKIKYRGTKGKADWEVDIENGNYDYLKADIDMD	240		
Db	181	NTSHNFKRWYHFDGTDWDSROLQNKIKYRGTKGKADWEVDIENGNYDYLKADIDMD	240		
Qy	241	HPEVINELRMWGVYNTLTNLIDGFRIDAVVHKIKSYTRDWLTHVRNTTGKMFVAEFWK	300		

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DB 241 HPEVINELEKMGWYNTNLNDGFRIDAVKHIKYSTRTDMLTHVRTTCKPFAVAEPFK 300
QY 301 NDLAALIENTKNTSMNSHVFDPVPLHYNLNASNSGYPFMRNLTNSGVQKPIHAVTFV 360
DB 301 NDLAALIENTKNTSMNSHVFDPVPLHYNLNASNSGYPFMRNLTNSGVQKPIHAVTFV 360
QY 361 DNHDSPGALBSFVQSWFEPFLAYAILTRRQGYPSVFGDYGIPTHGVPMSKSIDPL 420
DB 361 DNHDSPGALBSFVQSWFEPFLAYAILTRRQGYPSVFGDYGIPTHGVPMSKSIDPL 420
QY 421 LQARQYAYGTQDHYDPDHDIIIGTRRQGSHPNSGLATIMSDPGANKMYYGKHAQO 480
DB 421 LQARQYAYGTQDHYDPDHDIIIGTRRQGSHPNSGLATIMSDPGANKMYYGKHAQO 480
QY 481 VWRDITGNSGVTINADGWNFTVNGAVSVWVKQ 516
DB 481 VWRDITGNSGVTINADGWNFTVNGAVSVWVKQ 516

RESULT 2
AMT6_BACS7
ID AMT6_BACS7 STANDARD; PRT; 518 AA.
AC P19571;
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Glucan 1,4-alpha-maltohexaosidase precursor (EC 3.2.1.98) (G6-amy)ase)
DE (Maltotetraose-producing amylase) (Exo-maltohexahydrolase).
OS Bacillus sp. (strain 707).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
ON NCBI_TaxID=1416;
RX [1]
RX MEDLINE=88162814; PubMed=3258152;
RA Tsukamoto A., Kimura K., Ishii Y., Takano T., Yamane K.;
RT "Nucleotide sequence of the maltotetraose-producing amylase gene from
RT an alkalophilic Bacillus sp. #707 and structural similarity to
RT 11queyting type alpha-amyloses."
RL Biochem. Biophys. Res. Commun. 151:25-31(1988).
CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-D-glucosidic linkages
CC in amylose polysaccharides so as to remove successive
CC maltotetraose residues from the non-reducing chain ends.
CC -1- COFACTOR: Binds 2 calcium ions and 1 sodium ion per subunit (By
CC similarity).
CC -1- PATHWAY: Starch degradation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M18862; AAA22231.1; -.
DR PIR; A27705; A27705.
DR HSSP; P06278; 1VTS.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amyase; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amy; 1.
DR Carbohydrate metabolism; Direct protein sequencing; Glycosidase;
KM Hydrolyase; Signal.
FT SIGNAL 1 33
FT CHAIN 34 518 Glucan 1,4-alpha-maltohexaosidase.
FT ACT_SITE 269 269 Nucleophile (By similarity).
FT ACT_SITE 299 299 Proton donor (By similarity).
FT ACT_SITE 366 366 By similarity.

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FT METAL 139 139 Calcium 1 (By similarity).
FT METAL 196 196 Calcium 2 and sodium (By similarity).
FT METAL 219 219 Calcium 2 (via carbonyl oxygen) (By
FT METAL 221 221 similarity).
FT METAL 221 221 Calcium 2 and sodium (By similarity).
FT METAL 232 222 Calcium 1 and sodium (By similarity).
FT METAL 238 238 Calcium 1 and sodium (By similarity).
FT METAL 240 240 Calcium 2 (By similarity).
FT METAL 242 242 Calcium 2 (By similarity).
FT METAL 273 273 Calcium 1 (via carbonyl oxygen) (By
FT METAL 273 273 similarity).
SQ SEQUENCE 518 AA; 59009 MW; 3A961B21612682C4 CRC64;
Query Match 85.2%; Score 2438.5; DB 1; Length 518;
Best Local Similarity 83.7%; Pred. No. 2.6e-156;
Matches 426; Conservative 42; Mismatches 40; Indels 1; Gaps 1;
QY 8 ISVLLTLTLLAVLPLEPYMTPEAQAHHNGTGTMOYFEWHLPNDGNHNRLLDAAANLKS 67
DB 11 LSLILAFLLVITSI-PFTLLVDVEAHHNGTGTMOYFEWYLPNDGNHNRLLNSDANLKS 69
QY 68 KGITAVWIPPAWKGSQNDVGYGAYDLVDLGFENQKGYRTKYGRSOLQAVTSIKNG 127
DB 70 KGITAVWIPPAWKGSQNDVGYGAYDLVDLGFENQKGYRTKYGRSOLQAVTSIKNG 129
QY 128 IQYGGVYNNHKGADGTEMNVAIVNRSNOEISGEYTIAMTKFDPGRGNTSNFK 187
DB 130 IQYGGVYNNHKGADGTEMNVAIVNRSNOEISGEYTIAMTKFDPGRGNTSNFK 189
QY 188 KRWYHFDGTQDMSQLOKRIKFRGTGKAMWEVDIENGNYADIMYADIDMDHEVINE 247
DB 190 KRWYHFDGTQDMSQLOKRIKFRGTGKAMWEVDIENGNYADIMYADIDMDHEVINE 249
QY 248 LKNWGWYNTNLNDGFRIDAVKHIKYSTRTDMLTHVRTTCKPFAVAEPFKNDLALE 307
DB 250 LKNWGWYNTNLNDGFRIDAVKHIKYSTRTDMLTHVRTTCKPFAVAEPFKNDLALE 309
QY 308 NYLNTKSMNSHVFDPVPLHYNLNASNSGYPFMRNLTNSGVQKPIHAVTFDNDHDSOP 367
DB 310 NYLNTKSMNSHVFDPVPLHYNLNASNSGYPFMRNLTNSGVQKPIHAVTFDNDHDSOP 369
QY 368 GEALBSFVQSWFEPFLAYAILTRRQGYPSVFGDYGIPTHGVPMSKSIDPLQARQY 427
DB 370 GEALBSFVQSWFEPFLAYAILTRRQGYPSVFGDYGIPTHGVPMSKSIDPLQARQY 429
QY 428 AYTQHDYDPDHDIIIGTRRQGSHPNSGLATIMSDPGANKMYYGKHAQOQWPDITG 487
DB 430 AYTQHDYDPDHDIIIGTRRQGSHPNSGLATIMSDPGANKMYYGKHAQOQWPDITG 489
QY 488 NRTGVTINADGWNFTVNGAVSVWVKQ 516
DB 490 NRTGVTINADGWNFTVNGAVSVWVKQ 518

RESULT 3
ID Q59222 PRELIMINARY; PRT; 613 AA.
AC Q59222;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alpha-amyase (EC 3.2.2.1).
GN Name=Amy;
OS Bacillus sp. TS-23.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=38441;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TS-23;
RA Lin L.-D., Chu W.S., Hsu W.H.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
DR EMBL; U22045; AAA63900.1; -.

```

DR HSSP; P06279; 1HXV.
 DR GO; GO:0004556; F:alpha-amylase activity; IEA.
 DR GO; GO:0016798; F:hydrolyase activity, acting on glycosyl bonds; IEA.
 DR GO; GO:0008477; F:purine nucleosidase activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006047; Alpha_amyl_cat.
 DR InterPro; IPR006589; Alp_amyl_cat_sub.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR InterPro; IPR002044; Glyco_hydro_CBD.
 DR Pfam; PF00128; Alpha-amylase; 1.
 DR Pfam; PF00686; CBM_20; 1.
 DR PRINTS; PR00110; ALPHAAMYLAASE.
 DR PRODOM; PD001568; Glyco_hydro_CBD; 1.
 DR SMART; SM00642; Amy; 1.
 DR Glycosidase; Hydrolyase.
 SQ SEQUENCE 613 AA; 69536 MW; 14684A30FC2895EB CRC64;

Query Match 68.4%; Score 1958.5; DB 2; Length 613;
 Best Local Similarity 68.0%; Pred. No. 7.6e-124;
 Matches 344; Conservative 72; Mismatches 85; Indels 5; Gaps 3;

QY 9 SVLLTLIAVALEFPYTPERAOAHNGTNGTMOYFEWHLPNNGNHNRLRDAANLKS 68
 Db 12 SLIATLV--ISFFPFPST--AQANTAPINETMQYFEWDLPLNDGLTKVNGEANTSSL 67
 QY 69 GITVWVLPAMKGTSONDVGAYDLYDLGEFNQKGTVRTKXGTRSOLOQAVTSLKNGI 128
 Db 68 GITVWVLPAMKGTSONDVGAYDLYDLGEFNQKGTVRTKXGTRSOLOQAVTSLKNGI 127
 QY 129 QVYGDVVMNHKGADGTEMVAEVRNSNRNOEISGEYTIEMTKFDPFGKNTHSNPKW 188
 Db 128 QVYADVVENHKGADGTEFVDAVEVDPSNRNOETSCTIOQATKTFDPFGKNTYSSTKW 187
 QY 189 RWHFPGDGMDSQOLONKIYKFGTGKAMDEVDIENGNYDLYMADIDMDHEVINEL 248
 Db 188 RWHFPGDGMDSQOLONKIYKFGTGKAMDEVDIENGNYDLYMADIDMDHEVINEL 246
 QY 249 RWHFPGDGMDSQOLONKIYKFGTGKAMDEVDIENGNYDLYMADIDMDHEVINEL 248
 Db 249 RWHFPGDGMDSQOLONKIYKFGTGKAMDEVDIENGNYDLYMADIDMDHEVINEL 246
 QY 249 RWHFPGDGMDSQOLONKIYKFGTGKAMDEVDIENGNYDLYMADIDMDHEVINEL 248
 Db 249 RWHFPGDGMDSQOLONKIYKFGTGKAMDEVDIENGNYDLYMADIDMDHEVINEL 246
 QY 309 YLNTKSMNHVSFVDPLHYNLTNAASNGYFPMRNILNGSVVQKPHAVTFVNDHDSOPG 368
 Db 307 YLNTKSMNHVSFVDPLHYNLTNAASNGYFPMRNILNGSVVQKPHAVTFVNDHDSOPG 366
 QY 369 EALSFVQSWKPLAYALILTRREGYPSVFGDYGIPTHGVPMSKIDPLQAROTYA 428
 Db 367 QSLQSWKPLAYALILTRREGYPSVFGDYGIPTHGVPMSKIDPLQAROTYA 426
 QY 429 YGTHDVFDDHDIIGWTRREGDSHPNSGLATIMSDGPGKMMYVGGKKAQVWRDITGN 488
 Db 427 YGTRDVIDHDIIGWTRREGDSHPNSGLATIMSDGPGKMMYVGGKKAQVWRDITGN 486
 QY 489 RSGTFTINADGMGNTVNGAVSVYV 514
 Db 487 RSDTFTINADGMGNTVNGAVSVYV 512

RESULT 4
 081AS4 PRELIMINARY; PRT; 513 AA.
 AC 081AS4;
 DT 01-JUN-2003 (TReMBLrel. 24, Created)
 DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Glucan 1,4-alpha-maltohexaosidase (EC 3.2.1.98).
 GN OrderedlocusName=BC3482;
 OS Bacillus cereus (strain ATCC 14579 / DSM 31).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=226900;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;

RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
 RA Kapratel V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,
 RA Chu L., Mazur M., Goleman E., Larsen N., D'Souza M., Malinas T.,
 RA Grechkin Y., Pusch G., Haselkorn R., Fongstein M., Ehrlich S.D.,
 RA Overbeek R., Kyrides N.C.;
 RT "Genome sequence of Bacillus cereus and comparative analysis with
 RT Bacillus anthracis."
 RL Nature 423:87-91 (2003).
 DR EMBL; AE017009; AAP10417.1; -.
 DR HSSP; P06278; IVUS.
 DR GO; GO:0004556; F:alpha-amylase activity; IEA.
 DR GO; GO:0016798; F:hydrolyase activity, acting on glycosyl bonds; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006047; Alpha_amyl_cat.
 DR InterPro; IPR006589; Alp_amyl_cat_sub.
 DR Pfam; PF00128; Alpha-amylase; 1.
 DR SMART; SM00642; Amy; 1.
 DR Complete proteome; Glycosidase; Hydrolyase.
 SQ SEQUENCE 513 AA; 58306 MW; 05C4611C4BF9FP6 CRC64;

Query Match 68.4%; Score 1957.5; DB 2; Length 513;
 Best Local Similarity 67.7%; Pred. No. 7.2e-124;
 Matches 342; Conservative 67; Mismatches 91; Indels 5; Gaps 3;

QY 16 LAVALFPYTPERAOAHNGTNGTMOYFEWHLPNNGNHNRLRDAANLKS 74
 Db 10 LSVVFLPSIYEGSKAAYDLYVNGTLMQYFEWHPNDGNHNRLRDAANLKS 69
 QY 75 IIPAMKGTSONDVGAYDLYDLGEFNQKGTVRTKXGTRSOLOQAVTSLKNGI 134
 Db 70 IIPAYKGTTONDVGAYDLYDLGEFNQKGTVRTKXGTRSOLOQAVTSLKNGI 129
 QY 135 VNMHKGADGTEMVAEVRNSNRNOEISGEYTIEMTKFDPFGKNTHSNPKW 194
 Db 130 VNMHKGADGTEMVAEVRNSNRNOEISGEYTIEMTKFDPFGKNTYSSTKW 189
 QY 195 GTMDQSGROLONKIYKFGTGKAMDEVDIENGNYDLYMADIDMDHEVINEL 254
 Db 190 GTMDQSGROLONKIYKFGTGKAMDEVDIENGNYDLYMADIDMDHEVINEL 248
 QY 255 YLNTKSMNHVSFVDPLHYNLTNAASNGYFPMRNILNGSVVQKPHAVTFVNDHDSOPG 314
 Db 249 YLNTKSMNHVSFVDPLHYNLTNAASNGYFPMRNILNGSVVQKPHAVTFVNDHDSOPG 308
 QY 315 WNSVFPDPLHYNLTNAASNGYFPMRNILNGSVVQKPHAVTFVNDHDSOPG 374
 Db 309 WNSVFPDPLHYNLTNAASNGYFPMRNILNGSVVQKPHAVTFVNDHDSOPG 368
 QY 375 VQSWKPLAYALILTRREGYPSVFGDYGIPTHGVPMSKIDPLQAROTYA 431
 Db 369 VQSWKPLAYALILTRREGYPSVFGDYGIPTHGVPMSKIDPLQAROTYA 428
 QY 432 QHDFDHDHDIIGWTRREGDSHPNSGLATIMSDGPGKMMYVGGKKAQVWRDITGN 491
 Db 429 QHDFDHDHDIIGWTRREGDSHPNSGLATIMSDGPGKMMYVGGKKAQVWRDITGN 488
 QY 492 TTVTINADGMGNTVNGAVSVYV 516
 Db 489 TTVTINADGMGNTVNGAVSVYV 513

RESULT 5
 09A054 PRELIMINARY; PRT; 533 AA.
 AC 09A054;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Alpha-amylase.
 OS Bacillus megaterium.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1404;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Kim Y.B., Lee B.N., Son H.J., Lee J.W., Kim B.J., Kim Y.-W.,
 RA Park K.-H.;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF220440; AAK0598.1; -;
 DR HSSP; P06278; 1VJ5.
 DR GO; GO:0004556; F:alpha-amylase activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006047; Alpha amyl cat.
 DR InterPro; IPR006589; Alp_amy_cat_sub.
 DR Pfam; PF00128; Alpha-amylase; 1.
 DR SMART; SM00642; Amy; 1.
 SQ SEQUENCE 533 AA; 60557 MW; 789CECD6A19C7DDE CRC64;

Query Match 68.4%; Score 1957.5; DB 2; Length 533;
 Best Local Similarity 67.7%; Pred. No. 7.5e-124;
 Matches 342; Conservative 60; Mismatches 90; Indels 5; Gaps 3;

QY 16 LAVAVLFPYMTPEPAQAHNG-TNGTMMQYFEMHLPNDGNHNRRLRDAANLKSQITAAV 74
 DB LSVVMEFLPSIYGSKAYADTVNNGTLMQYFEWYAPNDGNHNRRLRDAENLQKIGITSW 89
 QY 75 IPPAMKGTSONDVGYGAYLDYDLGEFNQKGTVRTKIGTSOLQCAVTSLKNGIQYVGV 134
 DB IPPAYKGTQNDVGYGAYLDYDLGEFNQKGTVRTKIGTSOLQKSAIDLAKKNIIDYGV 149
 QY 135 VNMHKGADGTEWVNAVEVNRNNOISGEYTIEMTKEDPFGRGNTSHFKRWYHPD 194
 DB VNMHKGADGTEWVNAVEVNRNNOISGEYTIEMTKEDPFGRGNTSHFKRWYHPD 209
 QY 195 GTDMDSROLQNKIKYFRGTGKAMDEVDIENGNDYLYADIMDHPVINELRWGW 254
 DB GTDMDSRGL-NRIYKRGIGKAMDEVSSENGNDYLYADIMDHPVINELRWGW 268
 QY 210 GTDMDSRGL-NRIYKRGIGKAMDEVSSENGNDYLYADIMDHPVINELRWGW 268
 DB GTDMDSRGL-NRIYKRGIGKAMDEVSSENGNDYLYADIMDHPVINELRWGW 268
 QY 255 YNTNLMDGFRIDAVYHIGKSYTRDMLTHVRNTTGKMPFAVAFKNDLAIENYLNKTS 314
 DB YANELMDGFRIDAVYHIGKSYTRDMLTHVRNTTGKMPFAVAFKNDLAIENYLNKTS 328
 QY 269 YANELMDGFRIDAVYHIGKSYTRDMLTHVRNTTGKMPFAVAFKNDLAIENYLNKTS 328
 DB YANELMDGFRIDAVYHIGKSYTRDMLTHVRNTTGKMPFAVAFKNDLAIENYLNKTS 328
 QY 315 MNHVSFDPVPLHYNLVNASNGYFDMRNILNGSVQKPHAVTFPDNHSQPGALSEF 374
 DB YNOSVDFDAPLHYNLVNASNGYFDMRNILNGSVQKPHAVTFPDNHSQPGALSEF 388
 QY 329 YNOSVDFDAPLHYNLVNASNGYFDMRNILNGSVQKPHAVTFPDNHSQPGALSEF 388
 DB YNOSVDFDAPLHYNLVNASNGYFDMRNILNGSVQKPHAVTFPDNHSQPGALSEF 388
 QY 375 VQSMFKPLAYALLITREQGYPSVFGDYGI---PTHGVSMSKIDPLQARQYAYGT 431
 DB VQSMFKPLAYALLITREQGYPSVFGDYGI---PTHGVSMSKIDPLQARQYAYGT 448
 QY 389 VQSMFKPLAYALLITREQGYPSVFGDYGI---PTHGVSMSKIDPLQARQYAYGT 448
 DB VQSMFKPLAYALLITREQGYPSVFGDYGI---PTHGVSMSKIDPLQARQYAYGT 448
 QY 432 QHDFPHHDILGTRREGDSHPNSGLATIMSDFGCKMMYVYKAKAGVWRITGNRSG 491
 DB QHDFPHHDILGTRREGDSHPNSGLATIMSDFGCKMMYVYKAKAGVWRITGNRSG 508
 QY 449 QHDFPHHDILGTRREGDSHPNSGLATIMSDFGCKMMYVYKAKAGVWRITGNRSG 508
 DB QHDFPHHDILGTRREGDSHPNSGLATIMSDFGCKMMYVYKAKAGVWRITGNRSG 508
 QY 492 TVTINADGMGNFTVNGGAVSWWVK 516
 DB TVTINADGMGNFTVNGGAVSWWVK 533

RESULT 6

ID 081YJ4 PRELIMINARY; PRT; 513 AA.
 AC 081YJ4; 06HYU0; Q6K03; 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Alpha-amylase.
 GN Name:amyS; Ordered:locusNames=BA5351, BAS3291, GBA53551;
 OS Bacillus anthracis.
 OC Bacillales; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1392;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Ames / isolate Porton;
 RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
 RA Read T.D., Peterson S.N., Tourasse N.U., Bailly L.W., Paulsen I.T.,
 RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,

RA Holtzaple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,
 RA Kolonay J.F., Beaman M.U., Dodson R.J., Brinkac L.M., Gwinn M.L.,
 RA DeBoy R.T., Madpu R., Daugherty S.C., Dukin A.S., Haft D.H.,
 RA Nelson W.C., Peterson J.D., Pop M., Kouri H.M., Redune D.,
 RA Benton J.L., Mahmoud Y., Jiang L., Hance I.R., Weidman J.F.,
 RA Berry K.J., Platt R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
 RA Hazen A., Cline R.T., Redmond C., Thwaitte J.E., White O.,
 RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
 RA Hanna P.C., Koistice A.-B., Fraser C.M.;
 RA "The genome sequence of Bacillus anthracis Ames and comparison to
 RT closely related bacteria.";
 RL Nature 423:81-86(2003).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=Ames / isolate 0581;
 RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
 RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
 RA Fraser C.M.;
 RL "Bacillus anthracis comparative genomics.";
 RN Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 RN [3]

RP SEQUENCE FROM N.A.
 RC STRAIN=Scierne;
 RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
 RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
 RA Richardson P., Rubin E., Rice H.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB017035; AAP27311.1; -;
 DR EMBL; AB017334; AAP28659.1; -;
 DR EMBL; AB017225; AAP25599.1; -;
 DR HSSP; P06278; 1VJ5.
 DR TIGR; BA3551; -;
 DR TIGR; GBA3551; -;
 DR GO; GO:0004556; F:alpha-amylase activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006047; Alpha_amy_cat.
 DR InterPro; IPR006589; Alp_amy_cat_sub.
 DR Pfam; PF00128; Alpha-amylase; 1.
 DR SMART; SM00642; Amy; 1.
 KW Complete proteome.
 SQ SEQUENCE 513 AA; 58445 MW; 558D6EF282FD159B CRC64;

Query Match 68.2%; Score 1952.5; DB 2; Length 513;
 Best Local Similarity 67.1%; Pred. No. 1.6e-123;
 Matches 339; Conservative 72; Mismatches 89; Indels 5; Gaps 3;

QY 16 LAVAVLFPYMTPEPAQAHNG-TNGTMMQYFEMHLPNDGNHNRRLRDAANLKSQITAAV 74
 DB LSVVMEFLPSIYGSKAYADTVNNGTLMQYFEWYAPNDGNHNRRLRDAENLQKIGITSW 69
 QY 75 IPPAMKGTSONDVGYGAYLDYDLGEFNQKGTVRTKIGTSOLQCAVTSLKNGIQYVGV 134
 DB IPPAYKGTQNDVGYGAYLDYDLGEFNQKGTVRTKIGTSOLQKSAIDLAKKNIIDYGV 129
 QY 135 VNMHKGADGTEWVNAVEVNRNNOISGEYTIEMTKEDPFGRGNTSHFKRWYHPD 194
 DB VNMHKGADGTEWVNAVEVNRNNOISGEYTIEMTKEDPFGRGNTSHFKRWYHPD 189
 QY 195 GTDMDSROLQNKIKYFRGTGKAMDEVDIENGNDYLYADIMDHPVINELRWGW 254
 DB GTDMDSRGL-NRIYKRGIGKAMDEVSSENGNDYLYADIMDHPVINELRWGW 248
 QY 210 GTDMDSRGL-NRIYKRGIGKAMDEVSSENGNDYLYADIMDHPVINELRWGW 248
 DB GTDMDSRGL-NRIYKRGIGKAMDEVSSENGNDYLYADIMDHPVINELRWGW 248
 QY 255 YNTNLMDGFRIDAVYHIGKSYTRDMLTHVRNTTGKMPFAVAFKNDLAIENYLNKTS 314
 DB YANELMDGFRIDAVYHIGKSYTRDMLTHVRNTTGKMPFAVAFKNDLAIENYLNKTS 308
 QY 269 YANELMDGFRIDAVYHIGKSYTRDMLTHVRNTTGKMPFAVAFKNDLAIENYLNKTS 308
 DB YANELMDGFRIDAVYHIGKSYTRDMLTHVRNTTGKMPFAVAFKNDLAIENYLNKTS 308
 QY 315 MNHVSFDPVPLHYNLVNASNGYFDMRNILNGSVQKPHAVTFPDNHSQPGALSEF 374
 DB YNOSVDFDAPLHYNLVNASNGYFDMRNILNGSVQKPHAVTFPDNHSQPGALSEF 368
 QY 329 YNOSVDFDAPLHYNLVNASNGYFDMRNILNGSVQKPHAVTFPDNHSQPGALSEF 368
 DB YNOSVDFDAPLHYNLVNASNGYFDMRNILNGSVQKPHAVTFPDNHSQPGALSEF 368
 QY 375 VQSMFKPLAYALLITREQGYPSVFGDYGI---PTHGVSMSKIDPLQARQYAYGT 431
 DB VQSMFKPLAYALLITREQGYPSVFGDYGI---PTHGVSMSKIDPLQARQYAYGT 428

Qy 432 QHDFDHHDIIGWTRREGDSHPNSGLATIMSDPGCNKMYVKGKAKQVWRDITGNSG 491
Db 429 QRDYLDHEDVIGWTRREGDSVHANSGLATLISDGGSGKMDVGNKNAEVEHMDITGNQTN 488
Qy 492 TTTINADGKGNFTYNGAVSVWVKQ 516
Db 489 TTTINKDGMGQFHVSGGSVSIVVQ 513

RESULT 7

Q6HFU3 PRELIMINARY; PRT; 513 AA.
ID Q6HFU3
AC Q6HFU3;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Alpha-amylase (1,4-alpha-D-glucan glucanohydrolase) (EC 3.2.1.1).
GN Name=amyS; OrderedLocustNames=B19727_3261;
OS Bacillus thuringiensis (subsp. konkukian).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
CX NCBI_TaxID=180856;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97-27;
RA Bretzin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Ohtsuka R.,
RA Richardson P., Rubin E., Rice H.;
RA "Complete genome sequence of Bacillus thuringiensis 97-27.";
RL Submitted (JUN-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; AE017355; AAT60457.1;
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR00589; Alp_amyl_cat_sub.
DR Pfam; PF00128; Alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
DR Complete proteome.
SQ SEQUENCE 513 AA; 58342 MW; CA9683F6C31A26C3 CRC64;

Query Match 68.1%; Score 1948.5; DB 2; Length 513;
Best Local Similarity 66.9%; Pred. No. 2.9e-123;
Matches 338; Conservative 73; Mismatches 89; Indels 5; Gaps 3;
Qy 16 LAVAVLPEYTPRPAQAHNG--TNGTMMQYFEMHLNDGNHNRRLRDPDANKSGITVAV 74
Db 10 LSVVLPFPISTYGSKVVADTINNGTLMQYFEMVAPSDGNHNRRLRTDAENLAQKITSVW 69
Qy 75 IPPAMKGTSONDVGAVDYLGLGFNOKGTVRTYGTGRSOLQAVTSLKNNGIQVYGDV 134
Db 70 IPPAYKGTQNDVGAVDYLGLGFNOKGTVRTYGTGRSOLQAVTSLKNNGIQVYGDV 129
Qy 135 VMAHKGADGTEWYNAVEVNSNRNOEISGEYTI EAWTKFDPFGKGNTHSNFKRWYFD 194
Db 130 VMAHKGADGTEWYNAVEVNSNRNOEISGEYTI EAWTKFDPFGKGNTHSNFKRWYFD 189
Qy 195 GTMDOSROLOKNTYKRGCTKAMDWEVDINGVYDYMADIMDHEVINEILRWGVW 254
Db 190 GTMDDEBGRKL-NRIYKRGCTKAMDWEVSENGVYDYMADIMDHEVINEILRWGVW 248
Qy 255 YTTNLTLDGFRIDAVKHIKYSTRDMLTHVNTTGGKPFVAFAEPKNDLAIENYLVNTS 314
Db 249 YANLNLNDGFRIDAVKHIKHYSTRDMLTHVNTTGGKPFVAFAEPKNDLAIENYLVNTS 308
Qy 315 WNSHVFDPVPLHYNLVNSNSGTYFDMRNILNGSVVQKPIHAYTFVDNHDSPQEALESF 374
Db 309 YNGSVFDPVPLHYNLVNSNSGTYFDMRNILNGSVVQKPIHAYTFVDNHDSPQEALESF 368
Qy 375 VQSMFKPLAYVLLITREGYPSVYGGYGGI---PTHGVSMSKSKIDPLQARQTYAGT 431
Db 369 VSAFFKPLAYVLLITREGYPSVYGGYGGI---PTHGVSMSKSKIDPLQARQTYAGT 428
Qy 432 QHDFDHHDIIGWTRREGDSHPNSGLATIMSDPGCNKMYVKGKAKQVWRDITGNSG 491

Db 429 QRDYLDHEDVIGWTRREGDSVHANSGLATLISDGGSGKMDVGNKNAEVEHMDITGNQTN 488
Qy 492 TTTINADGKGNFTYNGAVSVWVKQ 516
Db 489 TTTINKDGMGQFHVSGGSVSIVVQ 513

RESULT 8

AMY_BACLI STANDARD; PRT; 512 AA.
ID AMY_BACLI
AC P06278; Q84171;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
glucanohydrolase) (BLA).
GN Name=amyS; Synonyms=amyL;
OS Bacillus licheniformis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
CX NCBI_TaxID=1402;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 27811;
RX MEDLINE=86111694; PubMed=2418011;
RA Yuuki T., Nomura T., Tezuka H., Tsuboi A., Yamagata H., Tsukagoshi N.,
RA Ueda S.;
RA "Complete nucleotide sequence of a gene coding for heat- and pH-stable
RT alpha-amylase of Bacillus licheniformis: comparison of the amino acid
RT sequences of three bacterial liquefying alpha-amylases deduced from
RL the DNA sequences.";
RL J. Biochem. 98:1147-1156(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86195857; PubMed=3009417;
RA Gray G.L., Mainzer S.E., Rey M.W., Lamsa M.H., Kindle K.L.,
RA Carmona C., Reuquadt C.;
RA "Structural genes encoding the thermophilic alpha-amylases of Bacillus
RT stearotheophilus and Bacillus licheniformis.";
RL J. Bacteriol. 166:635-643(1986).
RN [3]
RP SEQUENCE FROM N.A.
RA Shahnaseini M., Ziaei A.A., Ghaemi N., Pourbabaee A.A.;
RT "An unusual DNA sequence encoded a hyperthermostable alpha-amylase.";
RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-104 FROM N.A.
RX MEDLINE=84185455; PubMed=6609154;
RA Stephens M.A., Ortlepp S.A., Ollington J.F., McConnell D.J.;
RT "Nucleotide sequence of the 5' region of the Bacillus licheniformis
RT alpha-amylase gene: comparison with the B. amyloliquefaciens gene.";
RL J. Bacteriol. 158:369-372(1994).
RN [5]
RP SEQUENCE OF 1-29 FROM N.A.
RX MEDLINE=89213924; PubMed=2540150;
RA Loeide B.M., Chambliss G.H., McConnell D.J.;
RT "Bacillus licheniformis alpha-amylase gene, amyL, is subject to
RT promoter-independent catalytic repression in Bacillus subtilis.";
RL J. Bacteriol. 171:2435-2442(1989).
RN [6]
RP SEQUENCE OF 30-47.
RX MEDLINE=82098050; PubMed=6172419;
RA Kuhn H., Pletzke P.P., Lampen J.O.;
RT "N-terminal amino acid sequence of Bacillus licheniformis alpha-
RT amylase: comparison with Bacillus amyloliquefaciens and Bacillus
RT subtilis enzymes.";
RL J. Bacteriol. 149:372-373(1982).
RN [7]
RP MAPPING OF SUBSTRATE-BINDING SITE.
RX MEDLINE=21992788; PubMed=11997021; DOI=10.1016/S0014-5793(02)02649-2;
RA Kandra L., Gyemant G., Remenyik J., Hovanszki G., Liptak A.;
RT "Action pattern and substrate mapping of Bacillus licheniformis alpha-
RT amylase (Bla) with modified maltooligosaccharide substrates.";

FEBS Lett. 518:79-82(2002).

[8] RT STRAIN=ATCC 6598; Pubmed=2394736; DOI=10.1074/jbc.M212618200; Machius M., Declerck N., Huber R., Wiegand G., RT "Kinetic stabilization of Bacillus licheniformis alpha-amylase through introduction of hydrophobic residues at the surface." J. Biol. Chem. 278:11546-11553(2003).

RA Declerck N., Joyet P., Galliard C., Masson J.M.; RT "Use of amber suppressors to investigate the thermostability of Bacillus licheniformis alpha-amylase. Amino acid replacements at 6 RT histidine residues reveal a critical position at His-133." J. Biol. Chem. 265:15481-15488(1990).

RL J. Biol. Chem. 265:15481-15488(1990).

[9] RP MUTAGENESIS OF ALA-238. STRAIN=ATCC 6598; Pubmed=8771184; RT MEDLINE=96367070; DOI=10.1006/jmbi.2000.4025; RA Declerck N., Joyet P., Trosset J.Y., Garnier J., Galliard C.; RT "Hyperthermostable mutants of Bacillus licheniformis alpha-amylase: multiple amino acid replacements and molecular modelling." Protein Eng. 8:1029-1037(1995).

[10] RN MUTAGENESIS OF ASP-150; ASN-155; ARG-175; ASP-193; ASN-201; GLN-207; RP ASN-217; ASN-219; ASN-221; ASP-229; ASP-233; ALA-298; GLU-300; GLN-359 AND GLU-365. STRAIN=ATCC 6598; Pubmed=10966804; DOI=10.1006/jmbi.2000.4025; RC MEDLINE=20425100; DOI=10.1006/jmbi.2000.4025; RA Declerck N., Machius M., Wiegand G., Huber R., Galliard C.; RT "Probing structural determinants specifying high thermostability in Bacillus licheniformis alpha-amylase." J. Mol. Biol. 301:1041-1057(2000).

[11] RN MUTAGENESIS OF GLN-293 AND ASN-294. STRAIN=ATCC 6598; Pubmed=12736372; DOI=10.1093/proeng/gzq032; RC MEDLINE=22622182; DOI=10.1093/proeng/gzq032; RA Declerck N., Machius M., Joyet P., Wiegand G., Huber R., Galliard C.; RT "Hyperthermostabilization of Bacillus licheniformis alpha-amylase and modulation of its stability over a 50 degrees C temperature range." Protein Eng. 16:287-293(2003).

[12] RN MUTAGENESIS OF TRP-292 AND VAL-315. STRAIN=ATCC 27811; Pubmed=12915728; DOI=10.1093/proeng/gzq060; RC MEDLINE=22797417; DOI=10.1093/proeng/gzq060; RA Rivera M.H., Lopez-Munguia A., Soberon X., Saab-Rincon G.; RT "Alpha-amylase from Bacillus licheniformis mutants near to the catalytic site: effects on hydrolytic and transglycosylation activity." Protein Eng. 16:505-514(2003).

[13] RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS). STRAIN=ATCC 27811; Pubmed=7877175; RC MEDLINE=95182462; DOI=10.1016/S0969-2126(98)00032-X; RA Machius M., Wiegand G., Huber R.; RT "Crystal structure of calcium-depleted Bacillus licheniformis alpha-amylase at 2.2-A resolution." J. Mol. Biol. 246:545-559(1995).

[14] RN X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS). MEDLINE=98212915; Pubmed=9551551; DOI=10.1016/S0969-2126(98)00032-X; RA Machius M., Declerck N., Huber R., Wiegand G.; RT "Activation of Bacillus licheniformis alpha-amylase through a disorder-->order transition of the substrate-binding site mediated by a calcium-sodium-calcium metal triad." Structure 6:281-292(1998).

[15] RN X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 330-512. MEDLINE=20384196; Pubmed=10924103; DOI=10.1021/bi0000317; RA Brzozowski A.M., Lawton D.M., Turkemburg J.P., Bisgaard-Frantzen H., Svendsen A., Borchert T.V., Dauter Z., Wilson K.S., Davies G.J.; RT "Structural analysis of a chimeric bacterial alpha-amylase. High-resolution analysis of native and ligand complexes." Biochemistry 39:9099-9107(2000).

[16] RN X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF MUTANT H162V/N219F/A238V/Q293S/N294Y.

RC STRAIN=ATCC 6598; Pubmed=12540849; DOI=10.1074/jbc.M212618200; RX MEDLINE=22538505; DOI=10.1074/jbc.M212618200; RA Machius M., Declerck N., Huber R., Wiegand G., RT "Kinetic stabilization of Bacillus licheniformis alpha-amylase through introduction of hydrophobic residues at the surface." J. Biol. Chem. 278:11546-11553(2003).

RL J. Biol. Chem. 278:11546-11553(2003).

CC -1- CARBOLYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.

CC -1- COPACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.

CC -1- SUBUNIT: Monomer.

CC -1- BIOTECHNOLOGY: Used in the food industry for high temperature liquefaction of starch-containing mash and in the detergent industry to remove starch. Sold under the name Texamyl by Novozymes.

CC -1- MISCELLANEOUS: Able to work at relatively high (alkaline) pH values (up to pH 11) and at high temperatures (up to 100 degrees Celsius).

CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.

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CC EMBL: X03236; CAA26981.1; -

DR EMBL: M38570; AAA22228.1; -

DR EMBL: M3256; AAA22240.1; -

DR EMBL: K01984; AAA22193.1; -

DR EMBL: AF438149; AAO26743.1; -

DR EMBL: M26412; AAA22237.1; -

DR EMBL: A17930; CAA01355.1; -

DR PIR: A91997; ALBSL.

DR PDB: 1BD1; X-ray; @=30-512.

DR PDB: 1BP1; X-ray; A=30-218, B=219-512.

DR PDB: 1E3X; X-ray; A=-.

DR PDB: 1E34; X-ray; A=-.

DR PDB: 1E43; X-ray; A=-.

DR PDB: 1O80; X-ray; A=30-512.

DR PDB: 1VUS; X-ray; @=30-512.

DR InterPro: IPR006047; Alpha_ami1_cat.

DR InterPro: IPR006046; Glyco_hydro_13.

DR Pfam: PF00128; Alpha-amylase_1.

DR PRINTS: PR00110; ALPHAMYLASE.

KW 3D-structure; Calcium-binding; Carbohydrate metabolism; Signal.

KW Direct protein sequencing; Glycosidase; Hydrolase; Signal.

FT CHAIN 1 512 Alpha-amylase.

FT ACT_SITE 260 260 Nucleophile.

FT ACT_SITE 290 290 Proton donor.

FT ACT_SITE 357 357 By similarity.

FT METAL 133 133 Calcium 1.

FT METAL 190 190 Calcium 2 and sodium.

FT METAL 210 210 Calcium 2 (via carbonyl oxygen).

FT METAL 212 212 Calcium 2 and sodium.

FT METAL 223 223 Calcium 1 and sodium.

FT METAL 229 229 Calcium 1 and sodium.

FT METAL 231 231 Calcium 2.

FT METAL 233 233 Calcium 2.

FT METAL 264 264 Calcium 1 (via carbonyl oxygen).

FT METAL 329 329 Calcium 3 (via carbonyl oxygen).

Query Match 67.9%; Score 1942; DB 1; Length 512;

Best Local Similarity 66.6%; Pred. No. 8e-123;

Matches 347; Conservative 71; Mismatches 89; Indels 14; Gaps 5;

QY 1 MKAHRIISVLTLLAVAVLPFYMTPEPAQAHNGNGTGMQYFEHRLPNDGHNMRIRD 60

DB 1 MKQKRLVRLTLTLFLLFLLPHSAAAA---NINGTLMQYFEWMPNDGQHWKRLQW 56

Qy 61 DAANLKSQGTAAWIIPAMKGTSONDVGYGAYDLYDGEFNOGKTGRTKYSQLOQAV 120
 Db 57 DSAFLAHEGITAAMIIPAYKGTQADVGYGAYDLYDGEFNOGKTGRTKYSQLOQAV 116
 Qy 121 TSLKNGIIOYVGVVNMHKGADGTEMVNAVEVNRNSNNOISEGYTTEAATKDFPGRG 180
 Db 117 KSLSRDINIVYGDVIVNHKGADGTEMVNAVEVNRNSNNOISEGYTTEAATKDFPGRG 176
 Qy 181 NTHSNFKRWYHFGTMDGSRQLOKTIYKRGTKAMDEVDIENGNYDYLMTADIDMD 240
 Db 177 STYSDPFKWHYHFGTMDGSRQLOKTIYKRGTKAMDEVDIENGNYDYLMTADIDMD 233
 Qy 241 HPEYINELRWGVYVNTLNDGFRIDAVKHIIKYSYTRDMVLTHTYRNTGKMPFAVAFPMK 300
 Db 234 HPDVAIEIKRWGTAYANELQDGFRLDAVKHIIKYSYTRDMVLTHTYRNTGKMPFAVAFPMK 293
 Qy 301 NDLAIEINLYKTSWNSVDFVPLHYMLYNASNGYFDMKNIINGSVYVQKPIHAATFV 360
 Db 294 NDLAGLEINLYKTSWNSVDFVPLHYMLYNASNGYFDMKNIINGSVYVQKPIHAATFV 353
 Qy 361 DNHSQGEALLESVQSWFKPLAYALLITREOGTSPSYGYGIPHTG-----VPSMKS 415
 Db 354 DNHDTPQGSLESVQSWFKPLAYALLITREOGTSPSYGYGIPHTG-----VPSMKS 411
 Qy 416 KIDPLQARQTYAGTODHDFDHHDIIGWTRGSSHPNSGLATIMSDPGCNKMMYVYGK 475
 Db 412 KIEPILKARKOYAGTODHDFDHHDIIGWTRGSSHPNSGLATIMSDPGCNKMMYVYGK 471
 Qy 476 HKAGQVRDITGNRSQVTTINADGMNFTVNGAVSVVWQ 516
 Db 472 QNAGETWHDITGNRSQVTTINADGMNFTVNGAVSVVWQ 512

RESULT 9

Q65MX0 PRELIMINARY; PRT; 512 AA.
 AC Q65MX0; 25-OCT-2004 (Tremblrel. 28, Last sequence update)
 DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)
 DE Alpha-amylose (BC 3.2.1.1) (Trehalose-6-phosphate hydrolase).
 GN ORFNames=BL00499, BL100656;
 OS Bacillus licheniformis DSM 13.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=279010;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DSM 13;
 RX PubMed=15383718;
 RA Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,
 RA Ehrenreich P., Baumeister S., Henne A., Liesegang H., Weickl R.,
 RA Ehrenreich A., Gottschalk G.;
 RT "The Complete Genome Sequence of Bacillus licheniformis DSM13, an
 RT Organism with Great Industrial Potential";
 RL J. Mol. Microbiol. Biotechnol. 7:204-211 (2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 14580;
 RA Ray M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J.,
 RA Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen P.B.,
 RA Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S.,
 RA Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,
 RA Berka R.M.;
 RT "Complete genome sequence of the industrial bacterium Bacillus
 RT licheniformis and comparisons with closely related Bacillus species";
 RL Genome Biol. 5:R77-R77(2004).
 DR EMBL; AE017333; AAU39594.1; -
 DR EMBL; CP000002; AAU2245.1; -
 KW Glycosidase; Hydrolase
 SQ SEQUENCE 512 AA; 58529 MW; E3F8F560C3419D9D CRC64;

Query Match 67.6%; Score 1936; DB 2; Length 512;
 Best Local Similarity 66.4%; Pred. No. 2e-122;

Matches 346; Conservative 71; Mismatches 90; Indels 14; Gaps 5;
 Qy 1 MKNLRITSVLTLLAVAVLFPYMTPEPAQHNHGTGMMQYEMFLPNDGNMNLRD 60
 Db 1 MKQOKRLVYARLLPLFLFLIPHSAAAA---NLKGTLMQYEWMPNPGQMKRLQN 56
 Qy 61 DAANLKSQGTAAWIIPAMKGTSONDVGYGAYDLYDGEFNOGKTGRTKYSQLOQAV 120
 Db 57 DSAFLAHEGITAAMIIPAYKGTQADVGYGAYDLYDGEFNOGKTGRTKYSQLOQAV 116
 Qy 121 TSLKNGIIOYVGVVNMHKGADGTEMVNAVEVNRNSNNOISEGYTTEAATKDFPGRG 180
 Db 117 KSLSRDINIVYGDVIVNHKGADGTEMVNAVEVNRNSNNOISEGYTTEAATKDFPGRG 176
 Qy 181 NTHSNFKRWYHFGTMDGSRQLOKTIYKRGTKAMDEVDIENGNYDYLMTADIDMD 240
 Db 177 STYSDPFKWHYHFGTMDGSRQLOKTIYKRGTKAMDEVDIENGNYDYLMTADIDMD 233
 Qy 241 HPEYINELRWGVYVNTLNDGFRIDAVKHIIKYSYTRDMVLTHTYRNTGKMPFAVAFPMK 300
 Db 234 HPDVAIEIKRWGTAYANELQDGFRLDAVKHIIKYSYTRDMVLTHTYRNTGKMPFAVAFPMK 293
 Qy 301 NDLAIEINLYKTSWNSVDFVPLHYMLYNASNGYFDMKNIINGSVYVQKPIHAATFV 360
 Db 294 NDLAGLEINLYKTSWNSVDFVPLHYMLYNASNGYFDMKNIINGSVYVQKPIHAATFV 353
 Qy 361 DNHSQGEALLESVQSWFKPLAYALLITREOGTSPSYGYGIPHTG-----VPSMKS 415
 Db 354 DNHDTPQGSLESVQSWFKPLAYALLITREOGTSPSYGYGIPHTG-----VPSMKS 411
 Qy 416 KIDPLQARQTYAGTODHDFDHHDIIGWTRGSSHPNSGLATIMSDPGCNKMMYVYGK 475
 Db 412 KIEPILKARKOYAGTODHDFDHHDIIGWTRGSSHPNSGLATIMSDPGCNKMMYVYGK 471
 Qy 476 HKAGQVRDITGNRSQVTTINADGMNFTVNGAVSVVWQ 516
 Db 472 QNAGETWHDITGNRSQVTTINADGMNFTVNGAVSVVWQ 512

RESULT 10

Q9RQ78 PRELIMINARY; PRT; 519 AA.
 AC Q9RQ78; 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DE Raw starch digesting amylose precursor.
 OS Cytophaga sp.
 OC Bacteria; Bacteroidetes; Sphingobacteriales;
 OC Flexibacteraceae; Cytophaga.
 OX NCBI_TaxID=29535;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=22083510; PubMed=12089056;
 RX DOI=10.1128/AEM.68.7.3651-3654.2002;
 RA Jeang C.L., Chen L.S., Chen W.Y., Shiau R.J.;
 RT "Cloning of a gene encoding raw starch-digesting amylose from a
 RT Cytophaga sp. and its expression in Escherichia coli.";
 RL Appl. Environ. Microbiol. 68:3651-3654(2002).
 CC -1- SIMILARITY: Belong to family 13 of glycosyl hydrolases.
 DR EMBL; AF067653; AF00567.1; -
 DR HSSP; P00692; IE43;
 DR GO; GO:0004556; F:alpha-amylose activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006047; Alpha_amy1_cat.
 DR InterPro; IPR006589; Alp_amy1_cat_sub.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; Alpha-amylose; 1.
 DR PRINTS; PR00110; ALPHAMYLASE.
 DR SMART; SM00642; Amy; 1.
 KW Signal.
 FT SIGNAL 1 57 Potential.
 FT CHAIN 58 519 raw starch digesting amylose.

SQ SEQUENCE 519 AA; 56337 MW; 3E6B864ADF98B163 CRC64;
 Query Match 67.2%; Score 1923.5; DB 2; Length 519;
 Best Local Similarity 66.4%; Pred. No. 1.4e-121;
 Matches 340; Conservative 70; Mismatches 93; Indels 9; Gaps 3;

QY 8 ISVLTLLIAVAVLPYMTPEPAQAHNNGTNGTMQYFEMHLPDGNHNRRLDDAANKS 67
 Db 14 ITMFSTMLIV-----PSIAQPKAKAAATGTMTMOYFEMWVPNDGGQWNRRLRDAAYLS 68
 QY 68 KGLTAVWIPAMKGTSONDVGYGAYDLVDLGEFNQKGYRTKYGTSRLOAGATYSKNG 127
 Db 69 VGLTAVWTPPAYKGTSGADVGYGYDLYDLGEFNQKGYRTKYGTSRLOAGATYSKNG 128
 QY 128 IOYGVGVNHHKGGADGTEMNAVEVNSNRNOISGEYTIEMTKFDPGRGNTSHFK 187
 Db 129 IOYGVGVNHHKGGADGTEMNAVEVNSNRNOISGEYTIEMTKFDPGRGNTSHFK 188
 QY 188 WRVHFDGTWDSROLONKIYKFRGTGKAMDEVDIENGNYIYLMYADIDMDHPVINE 247
 Db 189 WQMFHFDGTWDSRSL-SRIKFRGTGKAMDEVSSENGNYIYLMYADIDYDHPVINE 247
 QY 248 LRMMGVWYNTLNLDFRIDAIVKHIKYSYTRDWLTHVRNTTGKPMFAVAFMKNDLAIE 307
 Db 248 MKKMGWYANEGVGLDGRIDAVKHIKYSFLKDWVNDNARATGKEMFTVGEYMGNDLGALN 307
 QY 308 NYLAKTSMNHSVPDPLHYNLYNANSNGYFDMENILNGSVQKPIHATVVDNHSQP 367
 Db 308 NYLAKVYNQSLFPAHLYNFYASTGGYDYDMENILNNTLVASNPFAATLVENHDTP 367
 QY 368 GEALIESVQSWFKPLAVALITREOGYPSYFGYV---GIPTHGVSSKSIDPILQAR 424
 Db 368 GQSLIESVQSWFKPLAVALITREOGYPSYFGYVGYGTYTTRPALSKIEPLKAR 427
 QY 425 QTVAYGTQHPDFDHDIIIGWTRGSSHPNSGLATIMSDPGGNKMMYVQKRAQGVWRD 484
 Db 425 KQVAYGTQHPDFDHDIIIGWTRGSSHPNSGLATIMSDPGGNKMMYVQKRAQGVWRD 487
 QY 485 ITGNRSGVTINADGMGNFTVNGAVSVWYQ 516
 Db 488 LTGNRTDKITIGSDGYATFPVNGSVSVWYQ 519

RESULT 11
 P71034 PRELIMINARY; PRT; 521 AA.
 AC P71034;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Alpha-amylose precursor.
 OS Bacillus sp. MK 716.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=54116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MK 716;
 RA Sidhu G.S., Chakrabarti T.,
 RL Submitted (OCT-1996) to the EMBL/Genbank/DBJ databases.
 CC -1 SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 DR EMBL; U75445; AAB18785.1; -
 DR HSPD; P06279; IHVX.
 DR GO; GO:0004556; F:alpha-amylose activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006047; Alpha_amy1_cat.
 DR InterPro; IPR006589; Alp_amy1_cat_sub.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; Alpha-amylose; 1.
 DR PRINTS; PR00110; ALPHAMYLASE.
 DR SMART; PR00110; ALPHAMYLASE.
 KW Signal.
 FT SIGNAL
 FT CHAIN 1 34 Potential.
 FT 35 521 alpha-amylose.

SQ SEQUENCE 521 AA; 59311 MW; 5612A8596D922E1 CRC64;
 Query Match 66.9%; Score 1915.5; DB 2; Length 521;
 Best Local Similarity 65.8%; Pred. No. 5e-121;
 Matches 340; Conservative 74; Mismatches 98; Indels 5; Gaps 3;

QY 1 MGLHNRITIS---VLTLLIAVAVLPYMTPEPAQAHNNGTNGTMQYFEMHLPDGNHNR 57
 Db 1 MLTFRIIRKGMFLALRLASLFCPPGQPAKA-AAFNGTMMQYFEMWLPDGTLTWK 59
 QY 58 LDDAANKSKGITAIVWIPAMKGTSONDVGYGAYDLVDLGEFNQKGYRTKYGTSRLO 117
 Db 60 VANEANNLSIGITLMLPPAYKGTSGADVGYDLYDLGEFNQKGYRTKYGTSRLO 119
 QY 118 GAVTSLKNGGIOYGVGVNHHKGGADGTEMNAVEVNSNRNOISGEYTIEMTKFDP 177
 Db 120 QALQAHAAQMVADVDFDHRGADGTEWDAVEVNSDRNOISGYIOQAMTKFDP 179
 QY 178 GRGNTSHNPKRMWYFDPGTWDSROLONKIYKFRGTGKAMDEVDIENGNYIYLMYADI 237
 Db 180 GRGNTSHNPKRMWYFDPGTWDSRKL-SRIKFRGTGKAMDEVDIENGNYIYLMYADL 238
 QY 238 DMHDEVINELRNWGVWYNTLNLDFRIDAIVKHIKYSYTRDWLTHVRNTTGKPMFAV 297
 Db 239 DMHDEVINELRNWGVWYNTLNLDFRIDAIVKHIKYSYTRDWLTHVRNTTGKPMFAV 298
 QY 298 FKNDLAALENYLNKTSNMHSVPDPLHYNLYNANSNGYFDMENILNGSVQKPIHATV 357
 Db 299 YMSYDINKHANTYNTKNGTMSLPDAPLANKFTASKSGAFLMRLTMTLMKQPTLAV 358
 QY 358 TFDNDHDSQGEALBSFVQSWFKPLAVALITREOGYPSYFGYVGYGTYTTRPALSKIE 417
 Db 359 TFDNDHDSQGEALBSFVQSWFKPLAVALITREOGYPSYFGYVGYGTYTTRPALSKIE 418
 QY 418 DPLQARQVYAYGTQHPDFDHDIIIGWTRGSSHPNSGLATIMSDPGGNKMMYVQKHX 477
 Db 419 DPLQARQVYAYGTQHPDFDHDIIIGWTRGSSHPNSGLATIMSDPGGNKMMYVQKHX 478
 QY 478 AGQVWRDITGNRSGVTINADGMGNFTVNGAVSVWY 514
 Db 479 AGQVWRDITGNRSGVTINADGMGNFTVNGAVSVWY 515

RESULT 12
 Q9KMY6 PRELIMINARY; PRT; 549 AA.
 AC Q9KMY6;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Alpha-amylose (EC 3.2.1.1).
 OS Bacillus stearothermophilus.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
 OX NCBI_TaxID=1422;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=US100;
 RA Ali M.B., Mirtl S., Merzghani M., Bejar S.,
 RT "Purification and sequence analysis of the atypical maltohexose-
 forming alpha-amylose of the B. stearothermophilus US100.",
 RL Enzyme Microb. Technol. 28:537-542(2001).
 CC -1 SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 DR EMBL; Y17557; CAB93517.1; -
 DR PIR; A54541; A54541.
 DR HSPD; P06279; IHVX.
 DR GO; GO:0004556; F:alpha-amylose activity; IEA.
 DR GO; GO:0016798; F:carbohydrate activity, acting on glycosyl bonds; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006047; Alpha_amy1_cat.
 DR InterPro; IPR006589; Alp_amy1_cat_sub.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; Alpha-amylose; 1.
 DR PRINTS; PR00110; ALPHAMYLASE.

DR SMART; SM00642; Aamy; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 549 AA; 62582 MW; 8DA3E66DF9120BCE CRC64;

Query Match 66.9%; Score 1915.5; DB 2; Length 549;
Best Local Similarity 65.8%; Pred. No. 5.3e-121;
Matches 340; Conservative 74; Mismatches 98; Indels 5; Gaps 3;

QY 1 MCLNRIIS---VLTLLLAVALFPVMTPEAQAHNHTNGTMQYFEMHLPNQGNHNR 57
DB 1 MLTHRIIRKGMWFLAFLTLASLFCPTGQAPKA-AAPFNGTMQYFEMWLPDDGTL 59
QY 58 LRDDAANLKSXGITAAMIIPAMKGTQNDVGYGAYDYLDELGNQKGTARTKGTGRS 117
DB 60 VANANNLSSIGITATMLPAPYKGTSRSDVGYDYLDELGNQKGTARTKGTGRS 119
QY 118 GAVTSLKNGIGQYGVDMNHKGADGTEMYNAVEVNSNRNOSIGETYTEAMTKFDP 177
DB 120 QAIQAAHAAGQVADVDFDHKGADGTEWDAVEVNSDRNOEISGTQIQAMTKFDP 179
QY 178 GRGHTHSFKRWYHFDGTDMDOSROLNKKYKPRGTGKAMDWEVDINGNYDILMY 237
DB 180 GRGHTYSFCKRWYHFDGVDWDESRKL-SRIYKRGIGKAMDWEVDINGNYDILMY 238
QY 238 DMDHPEVINELRNNGWYNTNLNDGFRIDAIVKHIKYSYTRDMLTHVANTTGKPF 297
DB 239 DMDHPEVTELMKMGKMYNTNIDGFRIDAVKHIKESFPDMLSYRSQTKPLFTYGE 298
QY 298 FPKNDLAIENYLNKTSWNHVSFDPVPLHYNLYNASNGYFDMRNILNGSVVQKPI 357
DB 299 YMSVDINLHNYIKTNGTMSLFDAPLNKRYTASKSGAFDMRTLMNTLMKQPTLAV 358
QY 358 TPNVNHDSQPEALSFQSWFKPLAYALITREGYSVYGYGIGPTHGVSMKSI 417
DB 359 TPNVNHDSQPEALSFQSWFKPLAYALITREGYSVYGYGIGPTHGVSMKSI 418
QY 418 DPLQARQTYAGTQHDYFDHDIIGWTRGDSHPNSGLATMSDGGKMKMYVYGK 477
DB 419 DPLIARDVAYGTOHDLHSDIIGWTRGDSHPNSGLATMSDGGKMKMYVYGK 478
QY 478 AGQYWRDITGNRSGTITINADGNGFTVNGAVSVW 514
DB 479 AGQYVYDLTGNRSDTITISDGMGEFKVNGSVSVW 515

RESULT 13
ID 031193 PRELIMINARY; PRT; 549 AA.
AC 031193;
DT 01-JAN-1998 (Tremblrel. 05. Created)
DT 01-JAN-1998 (Tremblrel. 05. Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25. Last annotation update)
DE Alpha amylase.
GN Name=ami;
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 31193;
RA da Silva A.C.R., Fernandes E., Pueyo M.T.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
DR EMBL; AF032864; AAB86961.1; -;
DR PIR; A54541; A54541.
DR HSSP; P06279; 1HVX.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR InterPro; IPR006047; Alpha-amyl_cat.
DR InterPro; IPR006589; Alp_ami_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAMYLASE.

DR SMART; SM00642; Aamy; 1.
SQ SEQUENCE 549 AA; 62651 MW; 2CA689EDACAD262 CRC64;

Query Match 66.9%; Score 1913.5; DB 2; Length 549;
Best Local Similarity 65.4%; Pred. No. 7.2e-121;
Matches 340; Conservative 72; Mismatches 97; Indels 11; Gaps 4;

QY 1 MCLNRIIS---VLTLLLAVALFPVMTPEAQAHNHTNGTMQYFEMHLPNQGNH 54
DB 1 MLTHRIIRKGMWFLAFLTLASLFCPTGHAAPAFNGTMQYFEMWLPDDGTL 56
QY 55 WNRLLRDAANLKSXGITAAMIIPAMKGTQNDVGYGAYDYLDELGNQKGTARTKGTGRS 114
DB 57 WTKYANENLSSIGITATMLPAPYKGTSRSDVGYDYLDELGNQKGTARTKGTGRS 116
QY 115 QLGAVTSLKNGIGQYGVDMNHKGADGTEMYNAVEVNSNRNOSIGETYTEAMTKF 174
DB 117 QYLAQIAHAAGQVADVDFDHKGADGTEWDAVEVNSDRNOEISGTQIQAMTKF 176
QY 175 DPGRGHTHSFKRWYHFDGTDMDOSROLNKKYKPRGTGKAMDWEVDINGNYDILMY 234
DB 177 DPGRGHTYSFCKRWYHFDGVDWDESRKL-SRIYKRGIGKAMDWEVDINGNYDILMY 235
QY 235 ADIDMDHPEVINELRNNGWYNTNLNDGFRIDAIVKHIKYSYTRDMLTHVANTTGKPF 294
DB 236 ADIDMDHPEVTELMKMGKMYNTNIDGFRIDAVKHIKESFPDMLSYRSQTKPLFT 295
QY 295 VAEFWKNDLAIENYLNKTSWNHVSFDPVPLHYNLYNASNGYFDMRNILNGSVVQKPI 354
DB 296 VGEYMSYDINLHNYIKTNGTMSLFDAPLNKRYTASKSGAFDMRTLMNTLMKQPT 355
QY 355 HAVTFVNHDSQPEALSFQSWFKPLAYALITREGYSVYGYGIGPTHGVSMKSI 414
DB 356 LAVTFVNHDSQPEALSFQSWFKPLAYALITREGYSVYGYGIGPTHGVSMKSI 415
QY 415 SKIDPLQARQTYAGTQHDYFDHDIIGWTRGDSHPNSGLATMSDGGKMKMYVYGK 474
DB 416 SKIDPLIARDVAYGTOHDLHSDIIGWTRGDSHPNSGLATMSDGGKMKMYVYGK 475
QY 475 KHKAGYWRDITGNRSGTITINADGNGFTVNGAVSVW 514
DB 476 KHKAGYVYDLTGNRSDTITISDGMGEFKVNGSVSVW 515

RESULT 14
ID AMY_BACST STANDARD; PRT; 549 AA.
AC P06279; Q45519;
DT 01-JAN-1988 (Rel. 06. Created)
DT 01-FEB-1996 (Rel. 33. Last sequence update)
DT 25-OCT-2004 (Rel. 45. Last annotation update)
DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase).
GN Name=amys;
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 35-39.
RC MEDLINE=65234394; PubMed=3924897;
RA Nakajima R., Imanaka T., Aiba S.;
RL "Nucleotide sequence of the Bacillus stearothermophilus alpha-amylase gene".
RN J. Bacteriol. 163:401-406(1985).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=DVS/PHI300;
RA MEDLINE=86008166; PubMed=3876333;
RA Ihara H., Sasaki T., Tsuboi A., Yamagata H., Tsukagoshi N., Ueda S.;
RT "Complete nucleotide sequence of a thermophilic alpha-amylase gene: homology between prokaryotic and eukaryotic alpha-amylases at the active sites".
RL J. Biochem. 98:95-103(1985).

RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=NZ-3;
RA MEDLINE=86195857; PubMed=3009417;
RA Gray G.L., Mainzer S.E., Rey M.W., Lamsa M.H., Kindle K.L.,
RA Carmona C., Reguete C.;
RT "Structural genes encoding the thermophilic alpha-amylases of *Bacillus*
RT *stearothermophilus* and *Bacillus licheniformis*.";
RL *J. Bacteriol.* 166:635-643(1986).
RN [4]
RP SEQUENCE FROM N.A.
RA Suominen I., Karp M., Lautamo J., Knowles J., Mantsaeslae P.;
RT "Thermotable alpha amylase of *Bacillus stearothermophilus*: cloning,
RT expression, and secretion by *Escherichia coli*.";
RL (in) Chaloupka J., Krumphanz V. (eds.);
RL Extracellular enzymes of microorganisms, pp.129-137, Plenum Press, New
RL York (1987).
RN [5]
RP SEQUENCE OF 1-122 FROM N.A., AND SEQUENCE OF 35-48.
RX STRAIN=DY-5;
RA MEDLINE=86059211; PubMed=2999073;
RA Tsukagoshi N., Iritani S., Sasaki T., Takemura T., Ihara H., Ito Y.,
RA Yamagata H., Ueda S.;
RT "Efficient synthesis and secretion of a thermophilic alpha-amylase by
RT protein-producing *Bacillus brevis* 47 carrying the *Bacillus*
RT *stearothermophilus* amylase gene.";
RL *J. Bacteriol.* 164:1182-1187(1985).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=21125602; PubMed=11226887;
RA Svud D., Fujimoto Z., Takase K., Matsumura M., Mizuno H.;
RT "Crystal structure of *Bacillus stearothermophilus* alpha-amylase:
RT possible factors determining the thermostability.";
RL *Biochem. J.* 253:461-468(2001).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.
CC -1- SUBUNIT: Monomer.
CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M11450; AAA22235.2; -;
DR EMBL: X02769; CAA26547.1; -;
DR EMBL: M57457; AAA22227.1; -;
DR EMBL: M13255; AAA22241.1; -;
DR PIR: A24436; A24436.
DR PIR: A91999; ALBSF.
DR PDB: 1HVX; X-ray; A=35-549.
DR InterPro: IPR006047; Alpha_amyl_cat.
DR InterPro: IPR006046; Glyco_hydro_13.
DR Pfam: PF00128; Alpha-amylase; 1.
DR PRINTS: PR00110; ALPHAMYLASE.
KW 3D-structure; Calcium-binding; Carbohydrate metabolism;
KW Direct protein sequencing; Glycosidase; Hydrolase; Signal.
FT STGMAL 1 34
FT CHAIN 1 34
FT ACT_SITE 35 549 Alpha-amylase.
FT ACT_SITE 268 268 Nucleophile.
FT ACT_SITE 298 298 Proton donor.
FT ACT_SITE 365 365
FT METAL 139 139 Calcium 1.
FT METAL 196 196 Calcium 2 and sodium.
FT METAL 218 218 Calcium 2 (via carbonyl oxygen).
FT METAL 220 220 Calcium 2 and sodium.
FT METAL 231 231 Calcium 1 and sodium.
FT METAL 237 237 Calcium 1 and sodium.
FT METAL 238 238 Sodium (via carbonyl oxygen).
FT METAL 238 238

FT METAL 239 239
FT METAL 272 272
FT METAL 337 337
FT METAL 339 339
FT METAL 440 440
FT METAL 441 441
FT METAL 464 464
FT CONFLICT 13 13
FT CONFLICT 19 19
FT CONFLICT 23 23
FT CONFLICT 31 31
FT CONFLICT 107 107
FT CONFLICT 167 167
FT CONFLICT 179 179
FT CONFLICT 251 251
FT CONFLICT 260 260
FT CONFLICT 284 284
FT CONFLICT 312 312
FT CONFLICT 338 338
FT CONFLICT 342 342
FT CONFLICT 346 346
FT CONFLICT 376 376
FT CONFLICT 526 526
FT CONFLICT 527 527
FT CONFLICT 535 535
FT STRAND 42 42
FT TURN 48 48
FT HELIX 56 56
FT TURN 69 69
FT TURN 70 70
FT STRAND 74 74
FT STRAND 82 82
FT TURN 86 86
FT TURN 87 87
FT STRAND 93 93
FT TURN 96 96
FT STRAND 104 104
FT TURN 105 105
FT STRAND 107 107
FT HELIX 115 115
FT TURN 128 128
FT STRAND 131 131
FT STRAND 140 140
FT STRAND 146 146
FT TURN 157 157
FT STRAND 159 159
FT STRAND 168 168
FT TURN 179 179
FT STRAND 183 183
FT STRAND 190 190
FT HELIX 192 192
FT STRAND 195 195
FT TURN 202 202
FT STRAND 206 206
FT TURN 215 215
FT TURN 226 226
FT STRAND 236 236
FT TURN 240 240
FT HELIX 243 243
FT STRAND 264 264
FT TURN 268 268
FT HELIX 270 270
FT TURN 272 272
FT HELIX 275 275
FT HELIX 277 277
FT STRAND 294 294
FT STRAND 304 304
FT TURN 314 314
FT HELIX 316 316
FT STRAND 319 319
FT HELIX 323 323
FT TURN 335 335
FT TURN 337 337
FT HELIX 341 341
FT TURN 344 344
FT HELIX 349 349
FT HELIX 354 354
FT STRAND 357 357
FT TURN 364 364
Calcium 2.
Calcium 1 (via carbonyl oxygen).
Calcium 3 (via carbonyl oxygen).
Calcium 3 (via carbonyl oxygen).
Calcium 3 (via carbonyl oxygen).
Calcium 3.
Calcium 3.
Calcium 3.
M -> V (in Ref. 3).
L -> W (in Ref. 3).
L -> S (in Ref. 2 and 3).
P -> H (in Ref. 2 and 3).
A -> T (in Ref. 2 and 5).
T -> I (in Ref. 2 and 3).
P -> N (in Ref. 4).
S -> N (in Ref. 2, 3 and 4).
TNI -> RTU (in Ref. 4).
D -> Y (in Ref. 2, 3 and 4).
M -> T (in Ref. 2 and 3).
T -> A (in Ref. 2 and 3).
R -> S (in Ref. 3).
T -> N (in Ref. 3).
V -> C (in Ref. 2 and 3).
WS -> RP (in Ref. 2).
S -> P (in Ref. 2).
D -> G (in Ref. 2 and 3).

```

FT TURN 368 369
FT TURN 371 372
FT TURN 378 380
FT HELIX 381 390
FT STRAND 395 399
FT HELIX 400 404
FT STRAND 406 406
FT HELIX 407 409
FT TURN 410 410
FT STRAND 411 411
FT HELIX 415 427
FT TURN 428 428
FT STRAND 433 436
FT STRAND 442 447
FT STRAND 450 450
FT TURN 451 452
FT STRAND 453 453
FT TURN 454 455
FT STRAND 458 463
FT STRAND 468 473
FT HELIX 476 478
FT TURN 479 480
FT STRAND 482 485
FT TURN 486 487
FT STRAND 493 495
FT TURN 498 499
FT STRAND 501 506

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Query Match 66.7%; Score 1908.5; DB 1; Length 549;
 Best Local Similarity 65.6%; Pred. No. 1.6e-120;
 Matches 339; Conservative 75; Mismatches 98; Indels 5; Gaps 3;

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QY 1 MTLNRRIIS---VLTLLLAVALPVMTEPQAHHNGTNGTMMQYFEMHLNDGNHNR 57
DB 1 MLTRRIIRKGMFLALFLTLFCPTGQPAKA-AAPNGTMMQYFEMYLPDDGLTWTK 59
QY 58 LRDDAANKSKGITAVWIPPAKGTSONDVGYGAYDLYDLGEFNOKGTVRTKYGTSOLO 117
DB 60 VANEANNLSIGITLWLPAPVKGTSRSDVGYGYDLYDLGEFNOKGAVRTKYGTKAYL 119
QY 118 GAVTSLKNGGIQVYGDVVMNHNKGADGTEMVNAVEVNSNRNOISGEYTIEMTKEDFP 177
DB 120 QAIQAAHAAGQVYADVVPFDHKGADGTEWDAVEVNSDRNOISGTYQIQAMTKEDFP 179
QY 178 GRGTHSFKRWYHFDGTDMDOSQOLNKTLYKFGCTGKAMDWEVDIENGNYDYIMYADI 237
DB 180 GRGNTYSSFKRWYHFDGTDMDOSQOLNKTLYKFGCTGKAMDWEVDIENGNYDYIMYADI 238
QY 238 DMDHEVINELRNNGWYNTNTLNDGPRIDAVKHKYSTRDMLTHVNTTGKMPFAVAE 297
DB 239 DMDHEVVELKSKGMWYNTNTLNDGPRIDAVKHKYSTRDMLTHVNTTGKMPFAVAE 298
QY 298 FPKNDLAIENYLNKTSWNHVSFVDFLHYNLYNASNGSGYFDMRNILNGSVVOKPIHAV 357
DB 299 YMSYDINKLHNYIKMTNGTMSLFPAPLNKFTYASKSGGTEDMRLNTMLKQPTLAV 358
QY 358 TFVNNHDSQBEALBSFQSWFKPLAYALLITREOGYTSVYGYDYIGPTHGVSMSKI 417
DB 359 TFVNNHDSQBEALBSFQSWFKPLAYALLITREOGYTSVYGYDYIGPTHGVSMSKI 418
QY 418 DPLLOAROTYVAGTOHDFDHDHDIIGWTRREGDSSHPNSGLATIMSDGSGKMMYVYGK 477
DB 419 DPLLIARDYVAGTOHDFDHDHDIIGWTRREGDSSHPNSGLATIMSDGSGKMMYVYGK 478
QY 478 AGQVWRDITGNRSGTITINADGMGNFTYNGAVSVWV 514
DB 479 AGQVYDITGNRSGTITINADGMGNFTYNGAVSVWV 515

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RESULT 15
 ID Q93148
 AC Q93148; PRELIMINARY; PRT; 501 AA.

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DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Amylase.
GN Name=amyK38;
OS Bacillus sp. KSM-K38.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxId=129736;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KSM-K38;
RX MEDLINE=21347468; PubMed=11453991;
RA Hagihara H., Hayashi Y., Endo K., Igataeshi K., Ozawa T., Kawai S.,
RA Ozaki K., Ito S.;
RT "deduced amino-acid sequence of a calcium-free alpha-amylase from a
RT strain of Bacillus: implications from molecular modeling of high
RT oxidation stability and chelator resistance of the enzyme.";
RL Eur. J. Biochem. 268:3974-3982(2001).
DR EMBL; AB051102; BAB71820.1; -.
DR PDB; 1UD2; X-ray; A=22-501.
DR PDB; 1UD3; X-ray; A=22-501.
DR PDB; 1UD4; X-ray; A=22-501.
DR PDB; 1UD5; X-ray; A=22-501.
DR PDB; 1UD6; X-ray; A=22-501.
DR PDB; 1UD8; X-ray; A=22-501.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha-amylase; 1.
DR Pfam; PF00128; Alpha-amylase; 1.
SQ SEQUENCE 501 AA; 57485 MW; 1240F46739A5C11 CRC64;

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Query Match 65.2%; Score 1866; DB 2; Length 501;
 Best Local Similarity 65.5%; Pred. No. 1e-117;
 Matches 329; Conservative 67; Mismatches 98; Indels 8; Gaps 3;

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QY 15 LLAVALPVMTEPQAHHNGTNGTMMQYFEMHLNDGNHNR LRDDAANKSKGITAVW 74
DB 8 MLAVLPFSPVVA-----DGLNGTMMQYFEMHLENQGHNR LRDDAANKSKGITAVW 62
QY 75 IPPAMKGTSONDVGYGAYDLYDLGEFNOKGTVRTKYGTSOLOQAVTSLKNGGIQVYGDV 134
DB 63 IPPAVKGSQADVGYGAYDLYDLGEFNOKGTVRTKYGTKALEBAISLKSNDINVGDV 122
QY 135 VMNHNKGADGTEMVNAVEVNSNRNOISGEYTIEMTKEDFPGRGTHSFKRWYHFD 194
DB 123 VMNHNKGADGTEMVNAVEVNSNRNOISGEYTIEMTKEDFPGRGTHSFKRWYHFD 182
QY 195 GTMDOSQOLNKTLYKFGCTGKAMDWEVDIENGNYDYIMYADI DMDHEVINELRNNGW 254
DB 183 GVDMDQ-RYQNNHLPFRANTY--MNMRYDEENGYDYILGSNIDFSHEVODELKMGSW 239
QY 255 YTNLTNDGPRIDAVKHKYSTRDMLTHVNTTGKMPFAVAE FPKNDLAIENYLNKTS 314
DB 240 FTDELDDGYRLDAIKHLPWYTSWVRHQENBQDLFFVGEYWKDVGALFELDEMN 299
QY 315 MNHVSFVDFLHYNLYNASNGSGYFDMRNILNGSVVOKPIHAVTFVNNHDSQBEALBSF 374
DB 300 MEMSLFVDFLHYNLYNASNGSGYFDMRNILNGSVVOKPIHAVTFVNNHDSQBEALBSF 359
QY 375 VQSWFKPLAYALLITREOGYTSVYGYDYIGPTHGVSMSKI DPLLOAROTYVAGTOH 434
DB 360 VADMFPLAYATLITREOGYTSVYGYDYIGPTHGVSMSKI DPLLIARDYVAGTOH 419
QY 435 YFDHDIIGWTRREGDSSHPNSGLATIMSDGSGKMMYVYGK AGQVWRDITGNRSGT 494
DB 420 YFDHMDVYGWTRREGSSRPNSGLATIMSDGSGKMMYVYGK AGQVYDITGNRSGT 479
QY 495 INADGMGNFTYNGAVSVWVQ 516
DB 480 INGDGMGEFTNGSVSVWVQ 501

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Search completed: May 2, 2005, 21:56:12

Thu May 5 18:22:56 2005

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Job time : 78 secs

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